

FIG. 1

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FIG.2A

M. catarrhalis strain 4223 λ EMBL3 clone 200kDa gene

ccatggatat gggcagggtgt gctgcctgc ogtatgatgg ogatgacacc ccatttgccc 60
catatctgta cgatttgaca tgtgatatga ttaacatgt gacatgattt aacattgttt 120
aatactgttg ccatcattac cataatttag taacgcattt agtaagocat ttgtaaaaat 180
cattgogccc ctttatgtgt atcatatgaa tagaatatta tgattgtatc tgattattgt 240
atcagaatgg tgatgctata tgatgatgoc tacgagttga tttggggttaa toactctatg 300
atttgatata ttttgaaact aatctattga cttaaatac cabatgggta taatttagca 360
taatggtagg ctttttgtta aaatcacatc gcaatattgt tctactgtta ctaccatgct 420
tgaatgacga tccaatacag cagattcatt caagtgatgt gtttgtatac gcaccattta 480
ccctaattat ttcaatcaaa tgcctatgtc agcatgtatc attttttaa ggtaaaccac 540
catgaaatcac atctataaaag tcatctttta caaagccaca ggcacattta tggcagtggc 600
agagtaagcc aaatcccaca gcacggggggg ggggtagctg tgctacaggg caagttggca 660

FIG. 2B

[illegible]

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FIG.2C

gcc atc ggt ggt gat gta aag gct agt ggt gat gcc tcg att gcc atc Ala Ile Gly Gly Asp Val Lys Ala Ser Gly Asp Ala Ser Ile Ala Ile	1004
85 90 95	
ggt agt gat gac tta cat ttg ctt gat cag cat ggt aat cct aaa cat Gly Ser Asp Asp Leu His Leu Leu Asp Gln His Gly Asn Pro Lys His	1052
100 105 110 115	
cog aaa ggt act ctg att aac gat ctt att aac ggc cat gca gta tta Pro Lys Gly Thr Leu Ile Asn Asp Leu Ile Asn Gly His Ala Val Leu	1100
120 125 130	
aaa gaa ata cga agc tca aag gat aat gat gta aaa tat aga cgc aca Lys Glu Ile Arg Ser Ser Lys Asp Asn Asp Val Lys Tyr Arg Arg Thr	1148
135 140 145	
acc gca agc gga cac gcc agt act gca gtg gga gcc atg tca tat gca Thr Ala Ser Gly His Ala Ser Thr Ala Val Gly Ala Met Ser Tyr Ala	1196
150 155 160	
cag ggt cat ttt tcc aac gcc ttt ggt aca cgg gca aca gct aaa agt Gln Gly His Phe Ser Ser Asn Ala Phe Gly Thr Arg Ala Thr Ala Lys Ser	1244
165 170 175	

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FIG.2D

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gcc tat tcc ttg gca gtg ggt ctt gcc gcc aca gcc gag gcc caa tct      1292
Ala Tyr Ser Leu Ala Val Gly Leu Ala Ala Thr Ala Glu Gly Gln Ser      195
180                               185      190
aca atc gct att ggt tct gat gca aca tct agc tog ttg gga gog ata      1340
Thr Ile Ala Ile Gly Ser Asp Ala Thr Ser Ser Ser Leu Gly Ala Ile      210
200                               205
gcc ctt ggt gca ggt act ogt gct cag cta cag gcc agt att gcc cta      1388
Ala Leu Gly Ala Gly Thr Arg Ala Gln Leu Gln Gly Ser Ile Ala Leu      225
215                               220
ggt caa ggt tct gtt gtc act cag agt gat aat aat tct aga cag gcc      1436
Gly Gln Gly Ser Val Val Thr Gln Ser Asp Asn Asn Ser Arg Pro Ala      240
230                               235
tat aca cca aat acc cag gca cta gac ccc aag ttt caa gcc acc aat      1484
Tyr Thr Pro Asn Thr Gln Ala Leu Asp Pro Lys Phe Gln Ala Thr Asn      255
245                               250
aat acg aag gog ggt cca ctt toc att ggt agt aac tct atc aaa cgt      1532
Asn Thr Lys Ala Gly Pro Leu Ser Ile Gly Ser Asn Ser Ile Lys Arg      275
260                               265

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FIG.2E

aaa atc atc aat gtc ggt gca ggt gtt aat aaa acc gat gcg gtc aat	1580
Lys Ile Ile Asn Val Gly Ala Gly Val Asn Lys Thr Asp Ala Val Asn	280 285 290
gtg gca cag cta gaa gcg gtg gtg aag tgg gct aag gag ggt aga att	1628
Val Ala Gln Leu Glu Ala Val Val Lys Trp Ala Lys Glu Arg Arg Ile	295 300 305
act ttt cag ggt gat gat aac agt act gac gta aaa ata ggt ttg gat	1676
Thr Phe Gln Gly Asp Asp Asn Ser Thr Asp Val Lys Ile Gly Leu Asp	310 315 320
aat act tta act att aaa ggt ggt gca gag acc aac gca tta acc gat	1724
Asn Thr Leu Thr Ile Lys Gly Gly Ala Glu Thr Asn Ala Leu Thr Asp	325 330 335
aat aat atc ggt gtg gta aaa gag gct gat aat agt ggt ctg aaa gtt	1772
Asn Asn Ile Gly Val Val Lys Glu Ala Asp Asn Ser Gly Leu Lys Val	340 345 350 355
aaa ctt gct aaa act tta aac aat ctt act gag gtg aat aca act aca	1820
Lys Leu Ala Lys Thr Leu Asn Asn Leu Thr Glu Val Asn Thr Thr Thr	360 365 370

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FIG.2F

tta aat gcc aca acc aca gtt aag gta ggt agt agt agt act aca	1868
Leu Asn Ala Thr Thr Thr Val Lys Val Gly Ser Ser Ser Thr Thr	
375 380 385	
gct gaa tta ttg agt gat agt tta acc ttt acc cag ccc aat aca ggc	1916
Ala Glu Leu Leu Ser Asp Ser Leu Thr Phe Thr Gln Pro Asn Thr Gly	
390 395 400	
agt caa agc aca agc aaa acc gtc tat ggc gtt aat ggg gtg aag ttt	1964
Ser Gln Ser Thr Ser Lys Thr Val Tyr Gly Val Asn Gly Val Lys Phe	
405 410 415	
act aat aat gca gaa aca aca gca gca atc ggc act act cgt att acc	2012
Thr Asn Asn Ala Glu Thr Thr Ala Ala Ile Gly Thr Thr Arg Ile Thr	
420 425 430 435	
aga gat aaa att ggc ttt gct cga gat ggt gat gtt gat gaa aaa caa	2060
Arg Asp Lys Ile Gly Phe Ala Arg Asp Gly Asp Val Asp Glu Lys Gln	
440 445 450	
gca cca tat ttg gat aaa aaa caa ctt aaa gtg ggt agt gtt gca att	2108
Ala Pro Tyr Leu Asp Lys Lys Gln Leu Lys Val Gly Ser Val Ala Ile	
455 460 465	

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FIG.2G

acc ata gac aat ggc att gat gca ggt aat aaa aag atc agt aat ctt	2156
Thr Ile Asp Asn Gly Ile Asp Ala Gly Asn Lys Lys Ile Ser Asn Leu	
470 475 480	
gcc aaa ggt agc agt gct aac gat gog gtt acc atc gaa cag ctc aaa	2204
Ala Lys Gly Ser Ser Ala Asn Asp Ala Val Thr Ile Glu Gln Leu Lys	
485 490 495	
gcc gcc aag cct act tta aac gca ggc gct ggc atc agt gtc aca cct	2252
Ala Ala Lys Pro Thr Leu Asn Ala Gly Ala Gly Ile Ser Val Thr Pro	
500 505 510 515	
act gaa ata tca gtt gat gct aag agt ggc aat gtt acc gcc cca act	2300
Thr Glu Ile Ser Val Asp Ala Lys Ser Gly Asn Val Thr Ala Pro Thr	
520 525 530	
tac aac att ggc gtg aaa acc acc gag ctt aac agt gat ggc act agt	2348
Tyr Asn Ile Gly Val Lys Thr Thr Glu Leu Asn Ser Asp Gly Thr Ser	
535 540 545	
gat aaa ttt agt gtt aag ggt agt ggt acg aac aat agc tta gtt acc	2396
Asp Lys Phe Ser Val Lys Gly Ser Gly Thr Asn Asn Ser Leu Val Thr	
550 555 560	

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FIG.2H

gcc gaa cat ttg gca agc tat cta aat gaa gtc aat cga acg gct gac 2444
 Ala Glu His Leu Ala Ser Tyr Leu Asn Glu Val Asn Arg Thr Ala Asp
 565 570 575

agt gct cta caa agc ttt acc gtt aaa gaa gaa gac gat gat gac gcc 2492
 Ser Ala Leu Gln Ser Phe Thr Val Lys Glu Glu Asp Asp Asp Ala
 580 585 590 595

aac gct atc acc gtg gct aaa gat acg aca aaa aat gcc ggc gca gtc 2540
 Asn Ala Ile Thr Val Ala Lys Asp Thr Thr Lys Asn Ala Gly Ala Val
 600 605 610

agc atc tta aaa ctc aaa ggt aaa aac ggt cta acg gtt gct acc aaa 2588
 Ser Ile Leu Lys Leu Lys Gly Lys Asn Gly Leu Thr Val Ala Thr Lys
 615 620 625

aaa gat ggt acg gtt acc ttt ggg ctt agc caa gat agc ggt ctg acc 2636
 Lys Asp Gly Thr Val Thr Phe Gly Leu Ser Gln Asp Ser Gly Leu Thr
 630 635 640

att ggc aaa agc acc cta aac aac gat ggc ttg act gtt aaa gat acc 2684
 Ile Gly Lys Ser Thr Leu Asn Asn Asp Gly Leu Thr Val Lys Asp Thr
 645 650 655

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FIG.2I

aac gaa caa atc caa gtc ggt gct aat ggc att aaa ttt act aat gtg	2732
Asn Glu Gln Ile Gln Val Gly Ala Asn Gly Ile Lys Phe Thr Asn Val	675
660	665
aat ggt agt aat cca ggt act ggc att gca aat acc gct cgc att acc	2780
Asn Gly Ser Asn Pro Gly Thr Gly Ile Ala Asn Thr Ala Arg Ile Thr	690
680	685
aga gat aaa att ggc ttt gct ggt tct gat ggt gca gtt gat aca aac	2828
Arg Asp Lys Ile Gly Phe Ala Gly Ser Asp Gly Ala Val Asp Thr Asn	705
695	700
aaa cct tat ctt gat caa gac aag cta caa gtt ggc aat gtt aag att	2876
Lys Pro Tyr Leu Asp Gln Asp Lys Leu Gln Val Gly Asn Val Lys Ile	720
710	715
acc aac act ggc att aac gca ggt ggt aaa gcc atc aca ggg ctg tcc	2924
Thr Asn Thr Gly Ile Asn Ala Gly Gly Lys Ala Ile Thr Gly Leu Ser	735
725	730
cca aca ctg cct agc att gcc gat caa agt agc cgc aac ata gaa ctg	2972
Pro Thr Leu Pro Ser Ile Ala Asp Gln Ser Ser Arg Asn Ile Glu Leu	755
740	745

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FIG.2J

ggc aat aca atc caa gac aaa gac aaa tcc aac gct gcc agc att aat 3020
 Gly Asn Thr Ile Gln Asp Lys Asp Lys Ser Asn Ala Ala Ser Ile Asn 770
 760
 gat ata tta aat aca ggc ttt aac cta aaa aat aat aac aac ccc att 3068
 Asp Ile Leu Asn Thr Gly Phe Asn Leu Lys Asn Asn Asn Pro Ile 785
 775 780
 gac ttt gtc tcc act tat gac att gtt gac ttt gcc aat ggc aat gcc 3116
 Asp Phe Val Ser Thr Tyr Asp Ile Val Asp Phe Ala Asn Gly Asn Ala 800
 795
 acc acc gcc aca gta acc cat gat acc gct aac aaa acc agt aaa gtg 3164
 Thr Thr Ala Thr Val Thr His Asp Thr Ala Asn Lys Thr Ser Lys Val 810
 805 815
 gta tat gat gtg aat gtg gat gat aca acc att cat cta aca ggc act 3212
 Val Tyr Asp Val Asn Val Asp Asp Thr Thr Ile His Leu Thr Gly Thr 830
 820 825 835
 gat gac aat aaa aaa ctt ggc gtc aaa acc acc aaa ctg aac aaa aca 3260
 Asp Asp Asn Lys Lys Leu Gly Val Lys Thr Thr Lys Leu Asn Lys Thr 840
 845 850

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FIG.2K

agt gct aat ggt aat aca gca act aac ttt aat gtt aac tct agt gat 3308
 Ser Ala Asn Gly Asn Thr Ala Thr Asn Phe Asn Val Asn Ser Ser Asp
 855 860 865

gaa gat gcc ctt gtt aac gcc aaa gac atc gcc gaa aat cta aac acc 3356
 Glu Asp Ala Leu Val Asn Ala Lys Asp Ile Ala Glu Asn Leu Asn Thr
 870 875 880

cta gcc aag gaa att cac acc acc aaa ggc aca gca gac acc gcc cta 3404
 Leu Ala Lys Glu Ile His Thr Thr Lys Gly Thr Ala Asp Thr Ala Leu
 885 890 895

caa acc ttt acc gtt aaa aag gta gat gaa aat aat gct gat gac 3452
 Gln Thr Phe Thr Val Lys Lys Val Asp Glu Asn Asn Ala Asp Asp
 900 905 910 915

gcc aac gcc atc acc gtg ggt caa aag aac gca aat aat caa gtc aac 3500
 Ala Asn Ala Ile Thr Val Gly Gln Lys Asn Ala Asn Asn Gln Val Asn
 920 925 930

acc cta aca ctc aaa ggt gaa aac ggt ctt aat att aaa acc gac aaa 3548
 Thr Leu Thr Leu Lys Lys Gly Glu Asn Gly Leu Asn Ile Lys Thr Asp Lys
 935 940 945

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FIG.2L

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aat ggt acg gtt acc ttt ggc att aac acc aca agc ggt ctt aaa gcc 3596
Asn Gly Thr Val Thr Phe Gly Ile Asn Thr Thr Ser Gly Leu Lys Ala
950 955 960

ggc aaa agc acc cta aac gac ggt ggc ttg tct att aaa aac ccc act 3644
Gly Lys Ser Thr Leu Asn Asp Gly Gly Leu Ser Ile Lys Asn Pro Thr
965 970 975

ggt agc gaa caa atc caa gtc ggt gct gat ggc gtg aag ttt gcc aag 3692
Gly Ser Glu Gln Ile Gln Val Gly Ala Asp Gly Val Lys Phe Ala Lys
980 985 990 995

gtt aat aat aat ggt gtt gta ggt gct ggc att gat ggc aca act cgc 3740
Val Asn Asn Asn Gly Val Val Gly Ala Gly Ile Asp Gly Thr Thr Arg
1000 1005 1010

att acc aga gat gaa att ggc ttt act ggg act aat ggc tca ctt gat 3788
Ile Thr Arg Asp Glu Ile Gly Phe Thr Gly Thr Asn Gly Ser Leu Asp
1015 1020 1025

aaa agc aaa ccc cac cta agc aaa gac ggc att aac gca ggt ggt aaa 3836
Lys Ser Lys Pro His Leu Ser Lys Asp Gly Ile Asn Ala Gly Gly Lys
1030 1035 1040

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FIG.2M

aag att acc aac att caa tca ggt gag att gcc caa aac agc cat gat	3884
Lys Ile Thr Asn Ile Gln Ser Gly Glu Ile Ala Gln Asn Ser His Asp	
1045 1050 1055	
gct gtg aca ggc ggc aag att tat gat tta aaa acc gaa ctt gaa aac	3932
Ala Val Thr Gly Gly Lys Ile Tyr Asp Leu Lys Thr Glu Leu Glu Asn	
1060 1065 1070 1075	
aaa atc agc agt act gcc aaa aca gca caa aac tca tta cac gaa ttc	3980
Lys Ile Ser Ser Thr Ala Lys Thr Ala Gln Asn Ser Leu His Glu Phe	
1080 1085 1090	
tca gta gca gat gaa caa ggt aat aac ttt acg gtt agt aac cct tac	4028
Ser Val Ala Asp Glu Gln Gly Asn Asn Phe Thr Val Ser Asn Pro Tyr	
1095 1100 1105	
tcc agt tat gac acc tca aag acc tct gat gtc atc acc ttt gca ggt	4076
Ser Ser Tyr Asp Thr Ser Lys Thr Ser Asp Val Ile Thr Phe Ala Gly	
1110 1115 1120	
gaa aac ggc att acc acc aag gta aat aaa ggt gtg cgt gtg ggc	4124
Glu Asn Gly Ile Thr Thr Lys Val Asn Lys Gly Val Val Arg Val Gly	
1125 1130 1135	

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FIG.2N

att gac caa acc aaa ggc tta acc acg cct aag ctg acc gtg ggt aat	4172
Ile Asp Gln Thr Lys Gly Leu Thr Thr Pro Lys Leu Thr Val Gly Asn	
1140 1145 1150 1155	
aat aat ggc aaa ggc att gtc att gac agc caa aat ggt caa aat acc	4220
Asn Asn Gly Lys Gly Ile Val Ile Asp Ser Gln Asn Gly Gln Asn Thr	
1160 1165 1170	
atc aca gga cta agc aac act cta gct aat gtt acc aat gat aaa ggt	4268
Ile Thr Gly Leu Ser Asn Thr Leu Ala Asn Val Thr Asn Asp Lys Gly	
1175 1180 1185	
agc gta cgc acc aca gaa cag ggc aat ata atc aaa gac gaa gac aaa	4316
Ser Val Arg Thr Thr Glu Gln Gly Asn Ile Ile Lys Asp Glu Asp Lys	
1190 1195 1200	
acc cgt gcc gcc agc att gtt gat gtg cta agc gca ggc ttt aac ttg	4364
Thr Arg Ala Ala Ser Ile Val Asp Val Leu Ser Ala Gly Phe Asn Leu	
1205 1210 1215	
caa ggc aat ggt gaa gcg gtt gac ttt gtc tcc act tat gac acc gtc	4412
Gln Gly Asn Gly Glu Ala Val Asp Phe Val Ser Thr Tyr Asp Thr Val	
1220 1225 1230 1235	

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FIG.20

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aac ttt gcc gat ggc aat gcc acc acc gct aag gtg acc tat gat gac      4460
Asn Phe Ala Asp Gly Asn Ala Thr Thr Ala Lys Val Thr Tyr Asp Asp      1240
                                     1245
aca agc aaa acc agt aaa gtg gtc tat gat gtc aat gtg gat gat aca      4508
Thr Ser Lys Thr Ser Lys Val Val Tyr Asp Val Asn Val Asp Asp Thr      1255
                                     1260
acc att gaa gtt aaa gat aaa aaa ctt ggc gta aaa acc acc aca ttg      4556
Thr Ile Glu Val Lys Asp Lys Lys Lys Leu Gly Val Lys Thr Thr Thr Leu      1270
                                     1275
acc agt act ggc aca ggt gct aat aaa ttt gcc cta agc aat caa gct      4604
Thr Ser Thr Gly Thr Gly Ala Asn Lys Phe Ala Leu Ser Asn Gln Ala      1285
                                     1290
act ggc gat gog ctt gtc aag gcc agt gat atc gtt gct cat cta aac      4652
Thr Gly Asp Ala Leu Val Lys Ala Ser Asp Ile Val Ala His Leu Asn      1300
                                     1305
acc tta tct ggc gac atc caa act gcc aaa ggg gca agc caa gog aac      4700
Thr Leu Ser Gly Asp Ile Gln Thr Ala Lys Gly Ala Ser Gln Ala Asn      1320
                                     1325

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FIG.2P

aac tca gca ggc tat gtg gat gct gat ggc aat aag gtc atc tat gac 4748
 Asn Ser Ala Gly Tyr Val Asp Ala Asp Gly Asn Lys Val Ile Tyr Asp
 1335 1340 1345

agt acc gat aac aag tac tat caa gcc aaa aat gat ggc aca gtt gat 4796
 Ser Thr Asp Asn Lys Tyr Tyr Gln Ala Lys Asn Asp Gly Thr Val Asp
 1350 1355 1360

aaa acc aaa gaa gtt gcc aaa gac aaa ctg gtc gcc caa gcc caa acc 4844
 Lys Thr Lys Glu Val Ala Lys Asp Lys Leu Val Ala Gln Ala Gln Thr
 1365 1370 1375

coa gat ggc aca ttg gct caa atg aat gtc aaa tca gtc att aac aaa 4892
 Pro Asp Gly Thr Leu Ala Gln Met Asn Val Lys Ser Val Ile Asn Lys
 1380 1385 1390 1395

gaa caa gta aat gat gcc aat aaa aag caa ggc atc aat gaa gac aac 4940
 Glu Gln Val Asn Asp Ala Asn Lys Lys Gln Gly Ile Asn Glu Asp Asn
 1400 1405 1410

gcc ttt gtt aaa gga ctt gaa aaa gcc gct tct gat aac aaa acc aaa 4988
 Ala Phe Val Lys Gly Leu Glu Lys Ala Ala Ser Asp Asn Lys Thr Lys
 1415 1420 1425

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FIG.2Q

aac gcc gca gta act gtg ggt gat tta aat gcc gtt gcc caa aca cag 5036
 Asn Ala Ala Val Thr Val Gly Asp Leu Asn Ala Val Ala Gln Thr Pro
 1430 1435 1440

ctg acc ttt gca ggg gat aca ggc aca acg gct aaa aaa ctg ggc gag 5084
 Leu Thr Phe Ala Gly Asp Thr Gly Thr Thr Ala Lys Lys Leu Gly Glu
 1445 1450 1455

act ttg acc atc aaa ggt ggg caa aca gac acc aat aag cta acc gat 5132
 Thr Leu Thr Ile Lys Gly Gly Gln Thr Thr Asp Thr Asn Lys Leu Thr Asp
 1460 1465 1470 1475

aat aac atc ggt gtg gta gca ggt act gat ggc ttc act gtc aaa ctt 5180
 Asn Asn Ile Gly Val Val Ala Gly Thr Asp Gly Phe Thr Val Lys Leu
 1480 1485 1490

gcc aaa gac cta acc aat ctt aac agc gtt aat gca ggt ggc acc aaa 5228
 Ala Lys Asp Leu Thr Asn Leu Asn Ser Val Asn Ala Gly Gly Thr Lys
 1495 1500 1505

att gat gac aaa ggc gtg tct ttt gta gac tca agc ggt caa gcc aaa 5276
 Ile Asp Asp Lys Gly Val Ser Phe Val Asp Ser Ser Gly Gln Ala Lys
 1510 1515 1520

FIG.2R

gca aac acc cct gtg cta agt gcc aat ggg ctg gac ctg ggt ggc aag 5324
 Ala Asn Thr Pro Val Leu Ser Ala Asn Gly Leu Asp Leu Gly Gly Lys
 1525 1530 1535

gtc atc agt aat gtg ggc aaa ggc aca aaa gat acc gac gct gcc aat 5372
 Val Ile Ser Asn Val Gly Lys Gly Thr Lys Asp Thr Asp Ala Ala Asn
 1540 1545 1550 1555

gta caa cag tta aac gaa gta cgc aac ttg ttg ggt ctt ggt aat gct 5420
 Val Gln Gln Leu Asn Glu Val Arg Asn Leu Leu Gly Leu Gly Asn Ala
 1560 1565 1570

ggt aat gat aac gct gac ggc aat cag gta aac att gcc gac atc aaa 5468
 Gly Asn Asp Asn Ala Asp Gly Asn Gln Val Asn Ile Ala Asp Ile Lys
 1575 1580 1585

aaa gac cca aat tca ggt tca tca tct aac cgc act gtc atc aaa gca 5516
 Lys Asp Pro Asn Ser Gly Ser Ser Ser Asn Arg Thr Val Ile Lys Ala
 1590 1595 1600

ggc acg gta ctt ggc ggt aaa ggt aat aac gat acc gaa aaa ctt gcc 5564
 Gly Thr Val Leu Gly Gly Lys Gly Asn Asn Asp Thr Glu Lys Leu Ala
 1605 1610 1615

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FIG.2S

act ggt ggt ata caa gtg ggc gtg gat aaa gac ggc aac gct aac ggc 5612
 Thr Gly Gly Ile Gln Val Gly Val Asp Lys Asp Gly Asn Ala Asn Gly
 1620 1625 1630 1635
 gat tta agc aat gtt tgg gtc aaa acc caa aaa gat ggc agc aaa aaa 5660
 Asp Leu Ser Asn Val Trp Val Lys Thr Gln Lys Asp Gly Ser Lys Lys
 1640 1645 1650
 gcc ctg ctc gcc act tat aac gcc gca ggt cag acc aac tat ttg acc 5708
 Ala Leu Leu Ala Thr Tyr Asn Ala Ala Gly Gln Thr Asn Tyr Leu Thr
 1655 1660 1665
 aac aac ccc gca gaa gcc att gac aga ata aat gaa caa ggt atc cgc 5756
 Asn Asn Pro Ala Glu Ala Ile Asp Arg Ile Asn Glu Gln Gly Ile Arg
 1670 1675 1680
 ttc ttc cat gtc aac gat ggc aat caa gag cct gtg gta caa ggg cgt 5804
 Phe Phe His Val Asn Asp Gly Asn Gln Glu Pro Val Val Gln Gly Arg
 1685 1690 1695
 aac ggc att gac tca agt gcc tca ggc aag cac tca gtg gcg ata ggt 5852
 Asn Gly Ile Asp Ser Ser Ala Ser Gly Lys His Ser Val Ala Ile Gly
 1700 1705 1710 1715

FIG.2T

ttc cag gcc aag gca gat ggt gaa gcc gcc gtt gcc ata ggc aga caa 5900
 Phe Gln Ala Lys Ala Asp Gly Glu Ala Ala Val Ala Ile Gly Arg Gln 1720 1725 1730

 acc caa gca gcc aac caa tcc atc gcc atc ggt gat aac gca caa gcc 5948
 Thr Gln Ala Gly Asn Gln Ser Ile Ala Ile Gly Asp Asn Ala Gln Ala 1735 1740 1745

 acg gcc gat caa tcc atc gcc atc ggt aca gcc aat gtg gta gca ggt 5996
 Thr Gly Asp Gln Ser Ile Ala Ile Gly Thr Gly Asn Val Val Ala Gly 1750 1755 1760

 aag cac tct ggt gcc atc gcc gac cca agc act gtt aag gct gat aac 6044
 Lys His Ser Gly Ala Ile Gly Asp Pro Ser Thr Val Lys Ala Asp Asn 1765 1770 1775

 agt tac agt gtg ggt aat aac aac cag ttt acc gat gcc act caa acc 6092
 Ser Tyr Ser Val Gly Asn Asn Gln Phe Thr Asp Ala Thr Gln Thr 1780 1785 1790 1795

 gat gtc ttt ggt gtg gcc aat aac atc acc gtg acc gaa agt aac tog 6140
 Asp Val Phe Gly Val Gly Asn Asn Ile Thr Val Thr Glu Ser Asn Ser 1800 1805 1810

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FIG.2U

gtt gcc tta ggt tca aac tct gcc atc agt gca ggc aca cac gca ggc 6188
 Val Ala Leu Gly Ser Asn Ser Ala Ile Ser Ala Gly Thr His Ala Gly 1815 1820 1825

 aca caa gcc aaa tct gac ggc aca gca ggt aca acc acc aca gca 6236
 Thr Gln Ala Lys Lys Ser Asp Gly Thr Ala Gly Thr Thr Thr Ala 1830 1835 1840

 ggt gca acc ggt acg gtt aaa ggc ttt gct gga caa acg gcg gtt ggt 6284
 Gly Ala Thr Gly Thr Val Lys Gly Phe Ala Gly Gln Thr Ala Val Gly 1845 1850 1855

 gcg gtc tcc gtg ggt gcc tca ggt gct gaa gcg cgt atc caa aat gtg 6332
 Ala Val Ser Val Gly Ala Ser Gly Ala Glu Arg Arg Ile Gln Asn Val 1860 1865 1870 1875

 gca gca ggt gag gtc agt gcc acc acc agc acc gat gcg gtc aat ggt agc 6380
 Ala Ala Gly Glu Val Ser Ala Thr Ser Thr Asp Ala Val Asn Gly Ser 1880 1885 1890

 cag ttg tac aaa gcc acc caa agc att gcc aac gca acc aat gag ctt 6428
 Gln Leu Tyr Lys Ala Thr Gln Ser Ile Ala Asn Ala Thr Asn Glu Leu 1895 1900 1905

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FIG.2V

gac cat cgt atc cac caa aac gaa aat aag gcc aat gca ggg att tca Asp His Arg Ile His Gln Asn Glu Asn Lys Ala Asn Ala Gly Ile Ser 1910 1915 1920	6476
tca gog atg gog atg gog tcc atg cca caa gcc tac att cct ggc aga Ser Ala Met Ala Met Ala Ser Met Pro Gln Ala Tyr Ile Pro Gly Arg 1925 1930 1935	6524
tcc atg gtt acc ggg ggt att gcc acc cac aac ggt caa ggt gog gtg Ser Met Val Thr Gly Gly Ile Ala Thr His Asn Gly Gln Gly Ala Val 1940 1945 1950 1955	6572
gca gtg gga ctg tog aag ctg tog gat aat ggt caa tgg gta ttt aaa Ala Val Gly Leu Ser Lys Leu Ser Asp Asn Gly Gln Trp Val Phe Lys 1960 1965 1970	6620
atc aat ggt tca gcc gat acc caa ggc cat gta ggg gog gca gtt ggt Ile Asn Gly Ser Ala Asp Thr Gln Gly His Val Gly Ala Ala Val Gly 1975 1980 1985	6668
gca ggt ttt cac ttt taagccataa atogcaagat ttactttaaa aatcaatctc Ala Gly Phe His Phe 1990	6723

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FIG.2W

accatagttg tataaaacag catcagcadc agtcatatta ctgatgctga tgttttttat 6783
cacttaaacc attttacgc tcaagtgatt ctctttcacc atgaccaaatt ogccattgat 6843
cataggtaaa cttattgagt aaattttatc aatgtagttg ttagatatgg ttaaaattgt 6903
gccattgacc aaaaatgac ogatttatcc ogaaaatttc tgattatgat cagttgacct 6963
gcaggtcgac 6973

FIG.3A

M. catarrhalis strain 4223 genomic 200kDa gene.

ccatggatat gggcaggtgt gctgcctgc ogtatgatgg ogatgacacc ccatttgccc 60
catatctgta ogatttgaca tgtgatatga tttaacatgt gacatgattt aacattgttt 120
aatactgttg ccatcattac cataatttag taacgcattt agtaacgcat ttgtaaaaaat 180
cattggcccc ctttatgtgt atcatatgaa tagaatatta tgattgtatc tgattattgt 240
atcagaatgg tgatgctata tgatgatgcc tacgagttga ttggggtaa tcactctatg 300
atttgatata ttttgaaact aatctattga cttaaatcac catatggta taatttagca 360
taatggtagg ctttttgtta aaatcacatc gcaatattgt tctactgtta ctaccatgct 420
tgaatgaoga tcccaatcac cagattcatt caagtgatgt gtttgtatcac gcaccattta 480
ccctaattat ttcaatcaaa tgcctatgtc agcatgtatc atttttttaa ggtaaaaccac 540
c atg aat cac atc tat aaa gtc atc ttt aac aaa gcc aca ggc aca ttt 589
Met Asn His Ile Tyr Lys Val Ile Phe Asn Lys Ala Thr Gly Thr Phe
1 5 10 15

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FIG.3B

atg gca gtg gca gag tac gcc aaa tcc cac agc acg ggg ggg ggt agc 637
 Met Ala Val Ala Glu Tyr Ala Lys Ser His Ser Thr Gly Gly Gly Ser
 20 25 30
 tgt gct aca ggg caa gtt ggc agt gta tgc act ctg agc ttt gcc cgt 685
 Cys Ala Thr Gly Gln Val Gly Ser Val Cys Thr Leu Ser Phe Ala Arg
 35 40 45
 att gcc gog ctc gct gtc ctc gtg atc ggt gca acg ctc agt ggc agt 733
 Ile Ala Ala Leu Ala Val Leu Val Ile Gly Ala Thr Leu Ser Gly Ser
 50 55 60
 gct tat gct caa aaa gat acc aaa cat atc gca att ggt gaa caa 781
 Ala Tyr Ala Gln Lys Lys Asp Thr Lys His Ile Ala Ile Gly Glu Gln
 65 70 75 80
 aac cag cca aga ogc tca ggc act gcc aag gog gac ggt gat oga gcc 829
 Asn Gln Pro Arg Arg Ser Gly Thr Ala Lys Ala Asp Gly Asp Arg Ala
 85 90 95
 att gct att ggt gaa aat gct aac gca cag ggc ggt caa gcc atc gcc 877
 Ile Ala Ile Gly Glu Asn Ala Asn Ala Gln Gly Gly Gln Ala Ile Ala
 100 105 110

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FIG.3C

atc ggt agt agt aat aaa act gtc aat gga agc agt ttg gat aag ata	925
Ile Gly Ser Ser Asn Lys Thr Val Asn Gly Ser Ser Leu Asp Lys Ile	125
115	120
ggt acc gat gct acg ggt caa gag tcc atc gcc atc ggt ggt gat gta	973
Gly Thr Asp Ala Thr Gly Gln Glu Ser Ile Ala Ile Gly Gly Asp Val	140
130	135
aag gct agt ggt gat gcc tog att gcc atc ggt agt gat gac tta cat	1021
Lys Ala Ser Gly Asp Ala Ser Ile Ala Ile Gly Ser Asp Asp Leu His	160
145	150
155	155
ttg ctt gat cag cat ggt aat cct aaa cat cog aaa ggt act ctg att	1069
Leu Leu Asp Gln His Gly Asn Pro Lys His Pro Lys Gly Thr Leu Ile	175
165	170
aac gat ctt att aac ggc cat gca gta tta aaa gaa ata cga agc tca	1117
Asn Asp Leu Ile Asn Gly His Ala Val Leu Lys Glu Ile Arg Ser Ser	190
180	185
aag gat aat gat gta aaa tat aga cgc aca acc gca agc gga cac gcc	1165
Lys Asp Asn Asp Val Lys Tyr Arg Arg Thr Thr Ala Ser Gly His Ala	205
195	200

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FIG.3D

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1213 agt act gca gtg gga gcc atg tca tat gca cag ggt cat ttt tcc aac
      Ser Thr Ala Val Gly Ala Met Ser Tyr Ala Gln Gly His Phe Ser Asn
      210 215 220
1261 gcc ttt ggt aca cgg gca aca gct aaa agt gcc tat tcc ttg gca gtg
      Ala Phe Gly Thr Arg Ala Thr Ala Lys Ser Ala Tyr Ser Leu Ala Val
      225 230 235 240
1309 ggt ctt gcc gcc aca gcc gag gcc caa tct aca atc gct att ggt tct
      Gly Leu Ala Ala Thr Ala Glu Gly Gln Ser Thr Ile Ala Ile Gly Ser
      245 250 255
1357 gat gca aca tct agc tog ttg gga gog ata gcc ctt ggt gca ggt act
      Asp Ala Thr Ser Ser Ser Leu Gly Ala Ile Ala Leu Gly Ala Gly Thr
      260 265 270
1405 cgt gct cag cta cag ggc agt att gcc cta ggt caa ggt tct gtt gtc
      Arg Ala Gln Leu Gln Gly Ser Ile Ala Leu Gly Gln Gly Ser Val Val
      275 280 285
1453 act cag agt gat aat aat tct aga cgg gcc tat aca cca aat acc cag
      Thr Gln Ser Asp Asn Asn Ser Arg Pro Ala Tyr Thr Pro Asn Thr Gln
      290 295 300

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FIG.3E

gca cta gac ccc aag ttt caa gcc acc aat aat acg aag gcg ggt cca 1501
 Ala Leu Asp Pro Lys Phe Gln Ala Thr Asn Asn Thr Lys Ala Gly Pro
 305 310 315 320
 ctt tcc att ggt agt aac tct atc aaa cgt aaa atc atc aat gtc ggt 1549
 Leu Ser Ile Gly Ser Asn Ser Ile Lys Arg Lys Ile Ile Asn Val Gly
 325 330 335
 gca ggt gtt aat aaa acc gat gcg gtc aat gtg gca cag cta gaa gcg 1597
 Ala Gly Val Asn Lys Thr Asp Ala Val Asn Val Ala Gln Leu Glu Ala
 340 345 350
 gtg gtg aag tgg gct aag gag cgt aga att act ttt cag ggt gat gat 1645
 Val Val Lys Trp Ala Lys Glu Arg Arg Ile Thr Phe Gln Gly Asp Asp
 355 360 365
 aac agt act gac gta aaa ata ggt ttg gat aat act tta act att aaa 1693
 Asn Ser Thr Asp Val Lys Ile Gly Leu Asp Asn Thr Leu Thr Ile Lys
 370 375 380
 ggt ggt gca gag acc aac gca tta acc gat aat aat atc ggt gtg gta 1741
 Gly Gly Ala Glu Thr Asn Ala Leu Thr Asp Asn Asn Ile Gly Val Val
 385 390 395 400

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FIG.3F

aaa gag gct gat aat agt ggt ctg aaa gtt aaa ctt gct aaa act tta	1789
Lys Glu Ala Asp Asn Ser Gly Leu Lys Val Lys Leu Ala Lys Thr Leu	405 410 415
aac aat ctt act gag gtg aat aca act aca tta aat gcc aca acc aca	1837
Asn Asn Leu Thr Glu Val Asn Thr Thr Leu Asn Ala Thr Thr Thr	420 425 430
ggt aag gta ggt agt agt agt act aca gct gaa tta ttg agt gat	1885
Val Lys Val Gly Ser Ser Ser Thr Thr Ala Glu Leu Leu Ser Asp	435 440 445
agt tta acc ttt acc cag ccc aat aca ggc agt caa agc aca agc aaa	1933
Ser Leu Thr Phe Thr Gln Pro Asn Thr Gly Ser Gln Ser Thr Ser Lys	450 455 460
acc gtc tat ggc gtt aat ggg gtg aag ttt act aat aat gca gaa aca	1981
Thr Val Tyr Gly Val Asn Gly Val Lys Phe Thr Asn Asn Ala Glu Thr	465 470 475 480
aca gca gca atc ggc act act cgt att acc aga gat aaa att ggc ttt	2029
Thr Ala Ala Ile Gly Thr Thr Arg Ile Thr Arg Asp Lys Ile Gly Phe	485 490 495

FIG.3G

gct cga gat ggt gat gtt gat gaa aaa caa gca cca tat ttg gat aaa	2077
Ala Arg Asp Gly Asp Val Asp Glu Lys Gln Ala Pro Tyr Leu Asp Lys	510
	500
aaa caa ctt aaa gtg ggt agt gtt gca att acc ata gac aat ggc att	2125
Lys Gln Leu Lys Val Gly Ser Val Ala Ile Thr Ile Asp Asn Gly Ile	525
	515
gat gca ggt aat aaa aag atc agt aat ctt gcc aaa ggt agc agt gct	2173
Asp Ala Gly Asn Lys Lys Ile Ser Asn Leu Ala Lys Gly Ser Ser Ala	540
	530
	535
aac gat gcg gtt acc atc gaa cag ctc aaa gcc gcc aag cct act tta	2221
Asn Asp Ala Val Thr Ile Glu Gln Leu Lys Ala Ala Lys Pro Thr Leu	560
	545
	550
	555
aac gca ggc gct ggc atc agt gtc aca cct act gaa ata tca gtt gat	2269
Asn Ala Gly Ala Gly Ile Ser Val Thr Pro Thr Glu Ile Ser Val Asp	575
	565
	570
gct aag agt ggc aat gtt acc gcc cca act tac aac att ggc gtg aaa	2317
Ala Lys Ser Gly Asn Val Thr Ala Pro Thr Tyr Asn Ile Gly Val Lys	590
	580
	585

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FIG.3H

acc acc gag ctt aac agt gat ggc act agt gat aaa ttt agt gtt aag	2365
Thr Thr Glu Leu Asn Ser Asp Gly Thr Ser Asp Lys Phe Ser Val Lys	
595 600 605	
ggg agt ggt acg aac aat agc tta gtt acc gcc gaa cat ttg gca agc	2413
Gly Ser Gly Thr Asn Asn Ser Leu Val Thr Ala Glu His Leu Ala Ser	
610 615 620	
tat cta aat gaa gtc aat oga acg gct gac agt gct cta caa agc ttt	2461
Tyr Leu Asn Glu Val Asn Arg Thr Ala Asp Ser Ala Leu Gln Ser Phe	
625 630 635 640	
acc gtt aaa gaa gaa gac gat gat gac gcc aac gct atc acc gtg gct	2509
Thr Val Lys Glu Glu Asp Asp Asp Ala Asn Ala Ile Thr Val Ala	
645 650 655	
aaa gat acg aca aaa aat gcc ggc gca gtc agc atc tta aaa ctc aaa	2557
Lys Asp Thr Thr Lys Asn Ala Glu Gly Ala Val Ser Ile Leu Lys Leu Lys	
660 665 670	
ggg aaa aac ggt cta acg gtt gct acc aaa aac gat ggt acg gtt acc	2605
Gly Lys Asn Gly Leu Thr Val Ala Thr Lys Lys Asp Gly Thr Val Thr	
675 680 685	

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FIG.3I

ttt ggg ctt agc caa gat agc ggt ctg acc att ggc aaa agc acc cta 2653
 Phe Gly Leu Ser Gln Asp Ser Gly Leu Thr Ile Gly Lys Ser Thr Leu
 690 700

aac aac gat ggc ttg act gtt aaa gat acc aac gaa caa atc caa gtc 2701
 Asn Asn Asp Gly Leu Thr Val Lys Asp Thr Asn Glu Gln Ile Gln Val
 705 710 715 720

ggt gct aat ggc att aaa ttt act aat gtg aat ggt agt aat cca ggt 2749
 Gly Ala Asn Gly Ile Lys Phe Thr Asn Val Asn Gly Ser Asn Pro Gly
 725 730 735

act ggc att gca aat acc gct cgc att acc aga gat aaa att ggc ttt 2797
 Thr Gly Ile Ala Asn Thr Ala Arg Ile Thr Arg Asp Lys Ile Gly Phe
 740 745 750

gct ggt tct gat ggt gca gtt gat aca aac aaa cct tat ctt gat caa 2845
 Ala Gly Ser Asp Gly Ala Val Asp Thr Asn Lys Pro Tyr Leu Asp Gln
 755 760 765

gac aag cta caa gtt ggc aat gtt aag att acc aac act ggc att aac 2893
 Asp Lys Leu Gln Val Gly Asn Val Lys Ile Thr Asn Thr Gly Ile Asn
 770 775 780

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FIG.3J

gca ggt ggt aaa gcc atc aca ggg ctg tcc cca aca ctg cct agc att 2941
 Ala Gly Gly Lys Ala Ile Thr Gly Leu Ser Pro Thr Leu Pro Ser Ile
 785 790 795 800

 gcc gat caa agt agc ogc aac ata gaa ctg ggc aat aca atc caa gac 2989
 Ala Asp Gln Ser Ser Arg Asn Ile Glu Leu Gly Asn Thr Ile Gln Asp
 805 810 815

 aaa gac aaa tcc aac gct gcc agc att aat gat ata tta aat aca ggc 3037
 Lys Asp Lys Ser Asn Ala Ala Ser Ile Asn Asp Ile Leu Asn Thr Gly
 820 825 830

 ttt aac cta aaa aat aat aac aac ccc att gac ttt gtc tcc act tat 3085
 Phe Asn Leu Lys Asn Asn Asn Asn Pro Ile Asp Phe Val Ser Thr Tyr
 835 840 845

 gac att gtt gac ttt gcc aat ggc aat gcc acc gcc acc gta acc 3133
 Asp Ile Val Asp Phe Ala Asn Gly Asn Ala Thr Thr Ala Thr Val Thr
 850 855 860

 cat gat acc gct aac aaa acc agt aaa gtg gta tat gat gtg aat gtg 3181
 His Asp Thr Ala Asn Lys Thr Ser Lys Val Val Tyr Asp Val Asn Val
 865 870 875 880

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FIG.3K

gat gat aca acc att cat cta aca ggc act gat gac aat aaa aaa ctt Asp Asp Thr Thr Ile His Leu Thr Gly Thr Asp Asp Asn Lys Lys Leu 885 890 895	3229
ggc gtc aaa acc acc aaa ctg aac aaa aca agt gct aat ggt aat aca Gly Val Lys Thr Thr Lys Leu Asn Lys Thr Ser Ala Asn Gly Asn Thr 900 905 910	3277
gca act aac ttt aat gtt aac tct agt gat gaa gat gcc ctt gtt aac Ala Thr Asn Phe Asn Val Asn Ser Ser Asp Glu Asp Ala Leu Val Asn 915 920 925	3325
gcc aaa gac atc gcc gaa aat cta aac acc cta gcc aag gaa att cac Ala Lys Asp Ile Ala Glu Asn Leu Asn Thr Leu Ala Lys Glu Ile His 930 935 940	3373
acc acc aaa ggc aca gca gac acc gcc cta caa acc ttt acc gtt aaa Thr Thr Lys Gly Thr Ala Asp Thr Ala Leu Gln Thr Phe Thr Val Lys 945 950 955 960	3421
aag gta gat gaa aat aat gct gat gac gcc aac gcc atc acc gtg Lys Val Asp Glu Asn Asn Ala Asp Ala Asn Ala Ile Thr Val 965 970 975	3469

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FIG.3L

ggt caa aag aac gca aat aat caa gtc aac acc cta aca ctc aaa ggt 3517
 Gly Gln Lys Asn Ala Asn Gln Val Asn Thr Leu Thr Leu Lys Gly 980 985 990

gaa aac ggt ctt aat att aaa acc gac aaa aat ggt acg gtt acc ttt 3565
 Glu Asn Gly Leu Asn Ile Lys Thr Asp Lys Asn Gly Thr Val Thr Phe 995 1000 1005

ggc att aac acc aca agc ggt ctt aaa gcc ggc aaa agc acc cta aac 3613
 Gly Ile Asn Thr Thr Ser Gly Leu Lys Ala Gly Lys Ser Thr Leu Asn 1010 1015 1020

gac ggt ggc ttg tct att aaa aac ccc act ggt agc gaa caa atc caa 3661
 Asp Gly Gly Leu Ser Ile Lys Asn Pro Thr Gly Ser Glu Gln Ile Gln 1025 1030 1035 1040

gtc ggt gct gat ggc gtg aag ttt gcc aag gtt aat aat ggt gtt 3709
 Val Gly Ala Asp Gly Val Lys Phe Ala Lys Val Asn Asn Asn Gly Val 1045 1050 1055

gta ggt gct ggc att gat ggc aca act cgc att acc aga gat gaa att 3757
 Val Gly Ala Gly Ile Asp Gly Thr Thr Arg Ile Thr Arg Asp Glu Ile 1060 1065 1070

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FIG.3M

ggc ttt act ggg act aat ggc tca ctt gat aaa agc aaa ccc cac cta	3805
Gly Phe Thr Gly Thr Asn Gly Ser Leu Asp Lys Ser Lys Pro His Leu	
1075	1080
1085	
agg aaa gac ggc att aac gca ggt ggt aaa aag att acc aac att caa	3853
Ser Lys Asp Gly Ile Asn Ala Gly Gly Lys Lys Ile Thr Asn Ile Gln	
1090	1095
1100	
toa ggt gag att gcc caa aac agc cat gat gct gtg aca ggc ggc aag	3901
Ser Gly Glu Ile Ala Gln Asn Ser His Asp Ala Val Thr Gly Gly Lys	
1105	1110
1115	1120
att tat gat tta aaa acc gaa ctt gaa aac aaa atc agc agt act gcc	3949
Ile Tyr Asp Leu Lys Thr Glu Leu Glu Asn Lys Ile Ser Ser Thr Ala	
1125	1130
1135	
aaa aca gca caa aac tca tta cac gaa ttc tca gta gca gat gaa caa	3997
Lys Thr Ala Gln Asn Ser Leu His Glu Phe Ser Val Ala Asp Glu Gln	
1140	1145
1150	
ggt aat aac ttt acg gtt agt aac cct tac tcc agt tat gac acc tca	4045
Gly Asn Asn Phe Thr Val Ser Asn Pro Tyr Ser Ser Tyr Asp Thr Ser	
1155	1160
1165	

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FIG.3N

aag acc tct gat gtc atc acc ttt gca ggt gaa aac ggc att acc acc 4093
 Lys Thr Ser Asp Val Ile Thr Phe Ala Gly Glu Asn Gly Ile Thr Thr
 1170 1175 1180

aag gta aat aaa ggt gtg gtg ogt gtg ggc att gac caa acc aaa ggc 4141
 Lys Val Asn Lys Gly Val Val Arg Val Gly Ile Asp Gln Thr Lys Gly
 1185 1190 1195 1200

tta acc acg cct aag ctg acc gtg ggt aat aat ggc aaa ggc att 4189
 Leu Thr Thr Pro Lys Lys Leu Thr Val Gly Asn Asn Gly Lys Gly Ile
 1205 1210 1215

gtc att gac agc caa aat ggt caa aat acc atc aca gga cta agc aac 4237
 Val Ile Asp Ser Gln Asn Gly Gln Asn Thr Ile Thr Gly Leu Ser Asn
 1220 1225 1230

act cta gct aat gtt acc aat gat aaa ggt agc gta cgc acc aca gaa 4285
 Thr Leu Ala Asn Val Thr Asn Asp Lys Gly Ser Val Arg Thr Thr Glu
 1235 1240 1245

cag ggc aat ata atc aaa gac gaa gac aaa acc cgt gcc gcc agc att 4333
 Gln Gly Asn Ile Ile Lys Asp Glu Asp Lys Thr Arg Ala Ala Ser Ile
 1250 1255 1260

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FIG.30

ggt gat gtg cta agc gca ggc ttt aac ttg caa ggc aat ggt gaa gcg Val Asp Val Leu Ser Ala Gly Phe Asn Leu Gln Gly Asn Gly Glu Ala 1265 1270 1275 1280	4381
ggt gac ttt gtc tcc act tat gac acc gtc aac ttt gcc gat ggc aat Val Asp Phe Val Ser Thr Tyr Asp Thr Val Asn Phe Ala Asp Gly Asn 1285 1290 1295	4429
gcc acc acc gct aag gtg acc tat gat gac aca agc aaa acc agt aaa Ala Thr Thr Ala Ala Lys Val Thr Tyr Asp Asp Thr Ser Lys Thr Ser Lys 1300 1305 1310	4477
gtg gtc tat gat gtc aat gtg gat gat aca acc att gaa gtt aaa gat Val Val Tyr Asp Val Asn Val Asp Asp Thr Thr Ile Glu Val Lys Asp 1315 1320 1325	4525
aaa aaa ctt ggc gta aaa acc acc aca ttg acc agt act ggc aca ggt Lys Lys Leu Gly Val Lys Thr Thr Thr Leu Thr Ser Thr Gly Thr Gly 1330 1335 1340	4573
gct aat aaa ttt gcc cta agc aat caa gct act ggc gat gcg ctt gtc Ala Asn Lys Phe Ala Leu Ser Asn Gln Ala Thr Gly Asp Ala Leu Val 1345 1350 1355 1360	4621

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FIG.3P

aag gcc agt gat atc gtt gct cat cta aac acc tta tct ggc gac atc 4669
 Lys Ala Ser Asp Ile Val Ala His Leu Asn Thr Leu Ser Gly Asp Ile 1375
 1365 1370

caa act gcc aaa ggg gca agc caa gcg aac aac tca gca ggc tat gtg 4717
 Gln Thr Ala Lys Gly Ala Ser Gln Ala Asn Ser Ala Gly Tyr Val 1390
 1380 1385

gat gct gat ggc aat aag gtc atc tat gac agt acc gat aac aag tac 4765
 Asp Ala Asp Gly Asn Lys Val Ile Tyr Asp Ser Thr Asp Asn Lys Tyr 1405
 1395 1400

tat caa gcc aaa aat gat ggc aca gtt gat aaa acc aaa gaa gtt gcc 4813
 Tyr Gln Ala Lys Asn Asp Gly Thr Val Asp Lys Thr Lys Glu Val Ala 1420
 1410 1415

aaa gac aaa ctg gtc gcc caa gcc caa acc cca gat ggc aca ttg gct 4861
 Lys Asp Lys Leu Val Ala Gln Ala Gln Thr Pro Asp Gly Thr Leu Ala 1440
 1425 1430 1435

caa atg aat gtc aaa tca gtc att aac aaa gaa caa gta aat gat gcc 4909
 Gln Met Asn Val Lys Ser Val Ile Asn Lys Glu Gln Val Asn Asp Ala 1455
 1445 1450

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FIG.3Q

aat aaa aag caa ggc atc aat gaa gac aac gcc ttt gtt aaa gga ctt	4957
Asn Lys Lys Gln Gly Ile Asn Glu Asp Asn Ala Phe Val Lys Gly Leu	
1460 1465 1470	
gaa aaa gcc gct tct gat aac aaa acc aaa aac gcc gca gta act gtg	5005
Glu Lys Ala Ala Ser Asp Asn Lys Thr Lys Asn Ala Ala Val Thr Val	
1475 1480 1485	
ggt gat tta aat gcc gtt gcc caa aca ccg ctg acc ttt gca ggg gat	5053
Gly Asp Leu Asn Ala Val Ala Gln Thr Pro Leu Thr Phe Ala Gly Asp	
1490 1495 1500	
aca ggc aca acg gct aaa aaa ctg ggc gag act ttg acc atc aaa ggt	5101
Thr Gly Thr Thr Ala Lys Lys Leu Gly Glu Thr Leu Thr Ile Lys Gly	
1505 1510 1515 1520	
ggg caa aca gac acc aat aag cta acc gat aat aac atc ggt gtg gta	5149
Gly Gln Thr Asp Thr Asn Lys Leu Thr Thr Asp Asn Ile Gly Val Val	
1525 1530 1535	
gca ggt act gat ggc ttc act gtc aaa ctt gcc aaa gac cta acc aat	5197
Ala Gly Thr Asp Gly Phe Thr Val Lys Leu Ala Lys Asp Leu Thr Asn	
1540 1545 1550	

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FIG.3R

ctt aac agc gtt aat gca ggt ggc acc aaa att gat gac aaa ggc gtg 5245
 Leu Asn Ser Val Asn Ala Gly Gly Thr Lys Ile Asp Asp Lys Gly Val
 1555 1560 1565

tct ttt gta gac tca agc ggt caa gcc aaa gca aac acc cct gtg cta 5293
 Ser Phe Val Asp Ser Ser Gly Gln Ala Lys Ala Asn Thr Pro Val Leu
 1570 1575 1580

agt gcc aat ggg ctg gac ctg ggt ggc aag gtc atc agt aat gtg ggc 5341
 Ser Ala Asn Gly Leu Asp Leu Gly Gly Lys Val Ile Ser Asn Val Gly
 1585 1590 1595 1600

aaa ggc aca aaa gat acc gac gct gcc aat gta caa cag tta aac gaa 5389
 Lys Gly Thr Lys Asp Thr Asp Ala Ala Asn Val Gln Gln Leu Asn Glu
 1605 1610 1615

gta cgc aac ttg ttg ggt ctt ggt aat gct ggt aat gat aac gct gac 5437
 Val Arg Asn Leu Leu Gly Leu Gly Asn Ala Gly Asn Asp Asn Ala Asp
 1620 1625 1630

ggc aat cag gta aac att gcc gac atc aaa aaa gac cca aat tca ggt 5485
 Gly Asn Gln Val Asn Ile Ala Asp Ile Lys Lys Asp Pro Asn Ser Gly
 1635 1640 1645

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FIG.3S

tca tct aac cgc act gtc atc aaa gca ggc acg gta ctt ggc ggt Ser Ser Asn Arg Thr Val Ile Lys Ala Gly Thr Val Leu Gly Gly 1650 1655 1660	5533
aaa ggt aat aac gat acc gaa aaa ctt gcc act ggt ggt ata caa gtg Lys Gly Asn Asn Asp Thr Glu Lys Leu Ala Thr Gly Gly Ile Gln Val 1665 1670 1675 1680	5581
ggc gtg gat aaa gac ggc aac gct aac ggc gat tta agc aat gtt tgg Gly Val Asp Lys Asp Gly Asn Ala Asn Gly Asp Leu Ser Asn Val Trp 1685 1690 1695	5629
gtc aaa acc caa aaa gat ggc agc aaa aaa gcc ctg ctc gcc act tat Val Lys Thr Gln Lys Asp Gly Ser Lys Lys Ala Leu Leu Ala Thr Tyr 1700 1705 1710	5677
aac gcc gca ggt cag acc aac tat ttg acc aac aac ccc gca gaa gcc Asn Ala Ala Gly Gln Thr Asn Tyr Leu Thr Asn Asn Pro Ala Glu Ala 1715 1720 1725	5725
att gac aga ata aat gaa caa ggt atc cgc ttc ttc cat gtc aac gat Ile Asp Arg Ile Asn Glu Gln Gly Ile Arg Phe Phe His Val Asn Asp 1730 1735 1740	5773

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FIG.3T

ggc aat caa gag cct gtg gta caa ggg cgt aac ggc att gac tca agt 5821
 Gly Asn Gln Glu Pro Val Val Gln Gly Arg Asn Gly Ile Asp Ser Ser
 1745 1750 1755 1760

gcc tca ggc aag cac tca gtg gog ata ggt ttc cag gcc aag gca gat 5869
 Ala Ser Gly Lys His Ser Val Ala Ile Gly Phe Gln Ala Lys Ala Asp
 1765 1770 1775

ggt gaa gcc gcc gtt gcc ata ggc aga caa acc caa gca ggc aac caa 5917
 Gly Glu Ala Ala Val Ala Ile Gly Arg Gln Thr Gln Ala Gly Asn Gln
 1780 1785 1790

tcc atc gcc atc ggt gat aac gca caa gcc aog ggc gat caa tcc atc 5965
 Ser Ile Ala Ile Gly Asp Asn Ala Gln Ala Thr Gly Asp Gln Ser Ile
 1795 1800 1805

gcc atc ggt aca ggc aat gtg gta gca ggt aag cac tct ggt gcc atc 6013
 Ala Ile Gly Thr Gly Asn Val Val Ala Gly Lys His Ser Gly Ala Ile
 1810 1815 1820

ggc gac cca agc act gtt aag gct gat aac agt tac agt gtg ggt aat 6061
 Gly Asp Pro Ser Thr Val Lys Ala Asp Asn Ser Tyr Ser Val Gly Asn
 1825 1830 1835 1840

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FIG.3U

aac aac cag ttt acc gat gcc act caa acc gat gtc ttt ggt gtg ggc Asn Asn Gln Phe Thr Asp Ala Thr Gln Thr Asp Val Phe Gly Val Gly	6109
1845 1850 1855	
aat aac atc acc gtg acc gaa agt aac tog gtt gcc tta ggt tca aac Asn Asn Ile Thr Val Thr Glu Ser Asn Ser Val Ala Leu Gly Ser Asn	6157
1860 1865 1870	
tct gcc atc agt gca ggc aca cac gca ggc aca caa gcc aaa aaa tct Ser Ala Ile Ser Ala Gly Thr His Ala Gly Thr Gln Ala Lys Lys Ser	6205
1875 1880 1885	
gac ggc aca gca ggt aca acc acc aca gca ggt gca acc ggt acg gtt Asp Gly Thr Ala Gly Thr Thr Thr Ala Gly Ala Thr Gly Thr Val	6253
1890 1895 1900	
aaa ggc ttt gct gga caa acg gog gtt ggt gog gtc tcc gtg ggt gcc Lys Gly Phe Ala Gly Gln Thr Ala Val Gly Ala Val Ser Val Gly Ala	6301
1905 1910 1915 1920	
tca ggt gct gaa cgc cgt atc caa aat gtg gca gca ggt gag gtc agt Ser Gly Ala Glu Arg Arg Ile Gln Asn Val Ala Ala Gly Glu Val Ser	6349
1925 1930 1935	

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FIG.3V

gcc acc agc acc gat gcg gtc aat ggt agc cag ttg tac aaa gcc acc 6397
 Ala Thr Ser Thr Asp Ala Val Asn Gly Ser Gln Leu Tyr Lys Ala Thr
 1940 1945 1950

 caa agc att gcc aac gca acc aat gag ctt gac cat ogc atc cac caa 6445
 Gln Ser Ile Ala Asn Ala Thr Asn Glu Leu Asp His Arg Ile His Gln
 1955 1960 1965

 aac gaa aat aag gcc aat gca ggg att tca tca gcg atg gcg atg gcg 6493
 Asn Glu Asn Lys Ala Asn Ala Gly Ile Ser Ser Ala Met Ala Met Ala
 1970 1975 1980

 toc atg cca caa gcc tac att cct gcc aga tcc atg gtt acc ggg ggt 6541
 Ser Met Pro Gln Ala Tyr Ile Pro Gly Arg Ser Met Val Thr Gly Gly
 1985 1990 1995 2000

 att gcc acc cac aac ggt caa ggt gcg gtg gca gtg gga ctg tog aag 6589
 Ile Ala Thr His Asn Gly Gln Gly Ala Val Ala Val Gly Leu Ser Lys
 2005 2010 2015

 ctg tog gat aat ggt caa tgg gta ttt aaa atc aat ggt tca gcc gat 6637
 Leu Ser Asp Asn Gly Gln Trp Val Phe Lys Ile Asn Gly Ser Ala Asp
 2020 2025 2030

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FIG.3W

acc caa ggc cat gta ggg gog gca gtt ggt gca ggt ttt cac ttt 6682
Thr Gln Gly His Val Gly Ala Ala Val Gly Ala Gly Phe His Phe
2035 2040 2045

taagccataa atogcaagat tt tacttaaa aatcaatctc accatagttg tataaaaacag 6742

catcagcatc agtcatatta ctgatgctga tgttttttat cacttaaac attttaccgc 6802

tcaagtgatt ctctttcacc atgaccaa atcggcattgat cataggtaaa cttattgagt 6862

aaattttatc aatgtagttg ttagatatgg ttaaaattgt gccattgacc aaaaaaatgac 6922

cgatttatcc ogaaaaattc tgattatgat cggttgacct gcagggtogac 6972

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FIG.4A

M. catarrhalis strain Q8 200kDa gene

48
 ATG aat cac atc tat aaa gtc atc ttt aac aaa gcc aca ggc aca ttt
 Met Asn His Ile Tyr Lys Val Ile Phe Asn Lys Ala Thr Gly Thr Phe
 1 5 10 15
 96
 atg gcc gtg gog gaa tat gcc aaa tcc cac agt acg ggg ggg ggt agc
 Met Ala Val Ala Glu Tyr Ala Lys Ser His Ser Thr Gly Gly Gly Ser
 20 25 30
 144
 tgt gct aca ggg caa gtt ggc agt gta ogc act cta agc ttt gcc cgt
 Cys Ala Thr Gly Gln Val Gly Ser Val Arg Thr Leu Ser Phe Ala Arg
 35 40 45
 192
 att gcc gog ctc gct gtc ctc gtg atc ggt gog acg ctc aat ggc agt
 Ile Ala Ala Leu Ala Val Leu Val Ile Gly Ala Thr Leu Asn Gly Ser
 50 55 60
 240
 gct tat gct caa caa att act acc aag atc gaa att ggt caa aca aac
 Ala Tyr Ala Gln Gln Ile Thr Thr Lys Ile Glu Ile Gly Gln Thr Asn
 65 70 75 80
 288
 aag ata aac aac acg ctg aaa ggc gat gcc cta gog aca ggt gaa gca
 Lys Ile Asn Asn Thr Leu Lys Lys Gly Asp Ala Leu Ala Thr Gly Glu Ala
 85 90 95

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FIG.4B

tcc att gct ttt ggt agt ctt tct aag gca caa ggc tct caa gct att	336
Ser Ile Ala Phe Gly Ser Leu Ser Lys Ala Gln Gly Ser Gln Ala Ile	110
100 105	
gct atc ggt agt gtc aaa cca gat cct aat aat ggt agt aat ggt aat	384
Ala Ile Gly Ser Val Lys Pro Asp Pro Asn Asn Gly Ser Asn Gly Asn	125
115 120	
gta ggt tcc cac gcc aaa ggt aac gag tcc atc gcc atc ggt ggt gat	432
Val Gly Ser His Ala Lys Gly Asn Glu Ser Ile Ala Ile Gly Gly Asp	140
130 135	
gta ttg gct gag ggt gat gcc tog att gcc atc ggt agt gat gac tta	480
Val Leu Ala Glu Gly Asp Ala Ser Ile Ala Ile Gly Ser Asp Asp Leu	160
145 150 155	
tat ttg cct aag aat ctt gat ctg aag aat gaa ttt cac aaa ctt att	528
Tyr Leu Pro Lys Asn Leu Asp Leu Lys Asn Glu Phe His Lys Leu Ile	175
165 170	
cat ggc cat gaa ata tta aaa ata caa acc tca acc gat ggt aaa	576
His Gly His Glu Ile Leu Lys Lys Ile Gln Thr Ser Thr Asp Gly Lys	190
180 185	

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FIG.4C

atc aaa tat cga cgc aca aga gca caa ggg cac gcc agt act gca gtg 624
 Ile Lys Tyr Arg Arg Thr Arg Ala Gln Gly His Ala Ser Thr Ala Val
 195 200 205

gga gcc atg tca tat gca cag ggt cat ttt tcc aac gcc ttt ggt aca 672
 Gly Ala Met Ser Tyr Ala Gln Gly His Phe Ser Asn Ala Phe Gly Thr
 210 215 220

tac gca aca gct gaa gct gcc tat tcc ttg gca gta ggt ctt gcc gcc 720
 Tyr Ala Thr Ala Glu Ala Ala Tyr Ser Leu Ala Val Gly Leu Ala Ala
 225 230 235 240

caa gcc aca aaa caa tct tca atc gct gtt ggt tcc aat gca aaa gct 768
 Gln Ala Thr Lys Gln Ser Ser Ile Ala Val Gly Ser Asn Ala Lys Ala
 245 250 255

aac gcg ttt gca gcg aca gcc att ggt gga aat act gta gtt aat ttg 816
 Asn Ala Phe Ala Ala Thr Ala Ile Gly Gly Asn Thr Val Val Asn Leu
 260 265 270

ggt cga ggc gtt gcc cta ggt ttt ggt tct cag atc ctt gat agg gat 864
 Gly Arg Gly Val Ala Leu Gly Phe Gly Ser Gln Ile Leu Asp Arg Asp
 275 280 285

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FIG.4D

aat aat aca gat gcc agt gcc tat gta cca cta ggt aaa acg tta gca 912
Asn Asn Thr Asp Ala Ser Ala Tyr Val Pro Leu Gly Lys Thr Leu Ala
290 295 300

gac cag tat aaa gcc acc cgc cag ggt gat tct acg gat ata ttt tcc 960
Asp Gln Tyr Lys Ala Thr Arg Gln Gly Asp Ser Thr Asp Ile Phe Ser
305 310 315 320

att ggt aat agt aat aat aat agc agt atc agg ogt aaa atc atc 1008
Ile Gly Asn Ser Asn Asn Asn Ser Ser Ile Arg Arg Lys Ile Ile
325 330 335

aat gtc ggt gcg ggt tct cgg gat acc gat gcg gtc aat gtg gca cag 1056
Asn Val Gly Ala Gly Ser Arg Asp Thr Asp Ala Val Asn Val Ala Gln
340 345 350

ctt aaa ttg gtg gag gaa ctg gct aat cgt aaa att act ttt aag ggt 1104
Leu Lys Leu Val Glu Glu Leu Ala Asn Arg Lys Ile Thr Phe Lys Gly
355 360 365

gat ggt gac aat aat agc aat agc gta gaa aga ggt ttg ggc aat act 1152
Asp Gly Asp Asn Asn Ser Asn Ser Val Glu Arg Gly Leu Gly Asn Thr
370 375 380

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FIG.4E

tta act att aaa ggt gat gca cag acc aac gca tta acc gaa gct aac Leu Thr Ile Lys Gly Asp Ala Gln Thr Asn Ala Leu Thr Glu Ala Asn 385 390 395 400	1200
atc ggt gtg gta aca gat ggc aat ggt ctg aaa gtt aaa ctt gct aaa Ile Gly Val Val Thr Asp Gly Asn Gly Leu Lys Val Lys Leu Ala Lys 405 410 415	1248
gag ctg act gga ttg acc agt gtc toc gct acc aac aaa atc acc gtt Glu Leu Thr Gly Leu Thr Ser Val Ser Ala Thr Asn Lys Ile Thr Val 420 425 430	1296
agt aat acc aac aac aac gcc gag cta caa agc ggt ggt ttg acc Ser Asn Thr Asn Asn Asn Ala Glu Leu Gln Ser Gly Gly Leu Thr 435 440 445	1344
ttt agc cca ata aca ggt aca aaa aca gat aaa acc gtc tac agc att Phe Ser Pro Ile Thr Gly Thr Lys Thr Asp Lys Thr Val Tyr Ser Ile 450 455 460	1392
gat gga ttg aag ttt act aat gat agt aat agt ata gca act aaa ggt Asp Gly Leu Lys Phe Thr Asn Asp Ser Asn Ser Ile Ala Thr Lys Gly 465 470 475 480	1440

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FIG.4F

act act cgt att acc aaa aag aaa att ggt ttt gct ggt act aat gat	1488
Thr Thr Arg Ile Thr Lys Lys Lys Ile Gly Phe Ala Gly Thr Asn Asp	
485 490 495	
gga gtt gat gaa agc aaa oct tat ctt gac aac gaa aag cta aaa gtt	1536
Gly Val Asp Glu Ser Lys Pro Tyr Leu Asp Asn Glu Lys Leu Lys Val	
500 505 510	
ggc aac agc acc cta aac agt ggt agc ttg act gtt aat aac acc act	1584
Gly Asn Ser Thr Leu Asn Ser Gly Ser Leu Thr Val Asn Asn Thr Thr	
515 520 525	
ggt aat aaa caa atc caa gtc ggt gct aat ggc att aaa ttt gcc aca	1632
Gly Asn Lys Gln Ile Gln Val Gly Ala Asn Gly Ile Lys Phe Ala Thr	
530 535 540	
gtc gct aat aat gtt gca aat acc tca gca aca gtc ggc act gct cgt	1680
Val Ala Asn Asn Val Ala Asn Thr Ser Ala Thr Val Gly Thr Ala Arg	
545 550 555 560	
att acc gaa gag aaa att ggt ttt gct ggt act aat gat gga gtt gat	1728
Ile Thr Glu Glu Lys Ile Gly Phe Ala Gly Thr Asn Asp Gly Val Asp	
565 570 575	

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FIG.4G

gaa caa gca cca tat ttg gat aaa gaa cga ctt aaa gtg ggt cgt gtt	1776
Glu Gln Ala Pro Tyr Leu Asp Lys Glu Arg Leu Lys Val Gly Arg Val	580 585 590
gaa att acc aca gat agt ggt att aat gct ggt aat cac aag att acc	1824
Glu Ile Thr Thr Asp Ser Gly Ile Asn Ala Gly Asn His Lys Ile Thr	595 600 605
gga ctt act aat ggt ata gca aat acc gat gog gtt acc atc aaa cag	1872
Gly Leu Thr Asn Gly Ile Ala Asn Thr Asp Ala Val Thr Ile Lys Gln	610 615 620
ctc aaa gac gcc aag cct act tta aac gca ggc gat ggc atc agt att	1920
Leu Lys Asp Ala Lys Pro Thr Leu Asn Ala Gly Asp Gly Ile Ser Ile	625 630 635 640
aat agt aat aac ggg gat cta gtt gat agt agt ggc aat att acc acc	1968
Asn Ser Asn Asn Gly Asp Leu Val Asp Ser Ser Gly Asn Ile Thr Thr	645 650 655
cca act tat aac att agc gtg aaa acc act aag ctt aac agt aat ggc	2016
Pro Thr Tyr Asn Ile Ser Val Lys Thr Thr Lys Leu Asn Ser Asn Gly	660 665 670

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FIG.4H

acc agt ggt aat aat aaa ttt agt gtt agt aat gct cat gat aac aat 2064
 Thr Ser Gly Asn Asn Lys Phe Ser Val Ser Asn Ala His Asp Asn Asn
 675 680 685

agc tta gtt acc gcc aaa gat ttg gca gac tat cta aat aaa gtc aat 2112
 Ser Leu Val Thr Ala Lys Asp Leu Ala Asp Tyr Leu Asn Lys Val Asn
 690 695 700

gaa acg gct gac agt gct cta cca agc ttt aaa gtc caa aac ggt gat 2160
 Glu Thr Ala Asp Ser Ala Leu Pro Ser Phe Lys Val Gln Asn Gly Asp
 705 710 715 720

aat agc aac aac gcc atc acc gtg ggt aaa gat aca aac ggc aag acc 2208
 Asn Ser Asn Asn Ala Ile Thr Val Gly Lys Asp Thr Asn Gly Lys Thr
 725 730 735

ttc aac acc tta aaa ctc aaa ggt gaa aac ggt gtt aat att acg acc 2256
 Phe Asn Thr Leu Lys Leu Lys Gly Glu Asn Gly Val Asn Ile Thr Thr
 740 745 750

aat aga gcc aca ggt aca gtt acc ttt ggc att gac caa agt aat ggt 2304
 Asn Arg Ala Thr Gly Thr Val Thr Phe Gly Ile Asp Gln Ser Asn Gly
 755 760 765

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FIG.4I

ctc acc acg cct aag ctg acc gtg ggt agc gat aca aat ggt aat cga	2352
Leu Thr Thr Pro Lys Leu Thr Val Gly Ser Asp Thr Asn Gly Asn Arg	
770 775 780	
ttg gtt att gag caa gtc cct agc gct gac ggt aac agc acc aaa aac	2400
Leu Val Ile Glu Gln Val Pro Ser Ala Asp Gly Asn Ser Thr Lys Asn	
785 790 795 800	
atc att aaa gga ttg tcc cca aca ctg cct agc att gcc agt cca agt	2448
Ile Ile Lys Gly Leu Ser Pro Thr Leu Pro Ser Ile Ala Ser Pro Ser	
805 810 815	
ggc cgc aac ata gca ctg ggc aat aca atc gaa gaa aaa gac aaa tcc	2496
Gly Arg Asn Ile Ala Leu Gly Asn Thr Ile Glu Glu Lys Asp Lys Ser	
820 825 830	
aac gct gcc agc att gat gat gtg cta aat gca ggc ttt aac cta aaa	2544
Asn Ala Ala Ser Ile Asp Asp Val Leu Asn Ala Gly Phe Asn Leu Lys	
835 840 845	
aat aat ggc aaa gac aaa gac ttt gtc tcc act tat gac act gtt gac	2592
Asn Asn Gly Lys Asp Lys Asp Phe Val Ser Thr Tyr Asp Thr Val Asp	
850 855 860	

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FIG.4J

ttt atc gat ggc aat gcc acc acc gcc aca gta act tat gat gaa gcc	2640
Phe Ile Asp Gly Asn Ala Thr Thr Ala Thr Val Thr Tyr Asp Glu Ala	
865 870 875 880	
aat caa acc agt aaa gtg gcg tat gat gtg aat gtg gat gag aaa acc	2688
Asn Gln Thr Ser Lys Val Ala Tyr Asp Val Asn Val Asp Glu Lys Thr	
885 890 895	
att gaa ctg aca ggc gat aat ggc aag aaa caa ctt ggc gtc aaa acc	2736
Ile Glu Leu Thr Gly Asp Asn Gly Lys Lys Gln Leu Gly Val Lys Thr	
900 905 910	
atc aaa ctg acc gaa aca agt act aat ggt aat gca act aca ttt agt	2784
Ile Lys Leu Thr Glu Thr Ser Thr Asn Gly Asn Ala Thr Thr Phe Ser	
915 920 925	
acc gac gat gac cat gcc ctt gtt aaa gcc agt gat atc gcc ggc aat	2832
Thr Asp Asp Asp His Ala Leu Val Lys Ala Ser Asp Ile Ala Gly Asn	
930 935 940	
cta aac acc cta gcc gag gaa att cac acc acc aaa ggc aca gca aac	2880
Leu Asn Thr Leu Ala Glu Glu Ile His Thr Thr Lys Gly Thr Ala Asn	
945 950 955 960	

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FIG.4K

acc gcc cta caa acc ttt acc gtt aaa aag gta gat gaa aat gat aag 2928
 Thr Ala Leu Gln Thr Phe Thr Val Lys Lys Val Asp Glu Asn Asp Lys 975
 965 970

gct gat gac acc aac gcc atc acc gtg ggt aaa gat ggc aca agt ggt 2976
 Ala Asp Asp Thr Asn Ala Ile Thr Val Gly Lys Asp Gly Thr Ser Gly 990
 980 985

aaa gtc aac acc tta aaa ctc aaa ggt aaa aac ggt ctt gat att aaa 3024
 Lys Val Asn Thr Leu Lys Leu Lys Gly Lys Asn Gly Leu Asp Ile Lys 1005
 995 1000

acc gac aaa gat ggt acg gtt acc ttt ggc att aac acc caa agc ggt 3072
 Thr Asp Lys Asp Gly Thr Val Thr Phe Gly Ile Asn Thr Gln Ser Gly 1020
 1010 1015

ctt aaa gcc ggc gac agc acc act cta aac aac aat ggc ttg tct att 3120
 Leu Lys Ala Gly Asp Ser Thr Thr Leu Asn Asn Asn Gly Leu Ser Ile 1040
 1025 1030 1035

aaa aac acc gct agt aac gaa caa atc caa gtc ggt gct gat ggc gtg 3168
 Lys Asn Thr Ala Ser Asn Glu Gln Ile Gln Val Gly Ala Asp Gly Val 1055
 1045 1050

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FIG.4L

aag ttt gcc atg gtt aat aat ggt gtt gta ggt gct ggc att gat ggc 3216
 Lys Phe Ala Met Val Asn Asn Gly Val Val Gly Ala Gly Ile Asp Gly
 1060 1065 1070

aca act cgc att acc aga gat gaa att ggc ttt act ggg act aat ggc 3264
 Thr Thr Arg Ile Thr Arg Asp Glu Ile Gly Phe Thr Gly Thr Asn Gly
 1075 1080 1085

tca ctt gat aaa agc aaa ccc cac cta agc aaa gac ggc att aac gca 3312
 Ser Leu Asp Lys Ser Lys Pro His Leu Ser Lys Asp Gly Ile Asn Ala
 1090 1095 1100

ggt ggt aaa aag att acc aac att caa tca ggt gag att gcc aaa aac 3360
 Gly Gly Lys Lys Ile Thr Asn Ile Gln Ser Gly Glu Ile Ala Lys Asn
 1105 1110 1115 1120

agc cat gat gct gtg aca ggc ggc aag att tat gat tta aaa acc gaa 3408
 Ser His Asp Ala Val Thr Gly Gly Lys Ile Tyr Asp Leu Lys Thr Glu
 1125 1130 1135

ctt gaa aat aaa atc agc agt act gcc aaa aca gca caa aac tca tta 3456
 Leu Glu Asn Lys Ile Ser Ser Thr Ala Lys Thr Ala Gln Asn Ser Leu
 1140 1145 1150

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FIG.4M

cac gaa ttc tca gta gca gat gaa caa ggt aat aac ttt acg gtt agt 3504
 His Glu Phe Ser Val Ala Asp Glu Gln Gly Asn Asn Phe Thr Val Ser
 1155 1160 1165

 aac cct tac toc agt tat gac acc tca aag acc tct gat gtc atc acc 3552
 Asn Pro Tyr Ser Ser Tyr Asp Thr Ser Lys Thr Ser Asp Val Ile Thr
 1170 1175 1180

 ttt gca ggt gaa aac ggc att acc acc aag gta aat aaa ggt gtg gtg 3600
 Phe Ala Gly Glu Asn Gly Ile Thr Thr Lys Val Asn Lys Gly Val Val
 1185 1190 1195 1200

 cgt gtg ggc att gac caa acc aaa ggc tta acc acg cct aag ctg acc 3648
 Arg Val Gly Ile Asp Gln Thr Lys Gly Leu Thr Thr Pro Lys Leu Thr
 1205 1210 1215

 gtg ggt aat aat aat ggc aaa ggc att gtc att aac agc caa aat ggt 3696
 Val Gly Asn Asn Asn Gly Lys Gly Ile Val Ile Asn Ser Gln Asn Gly
 1220 1225 1230

 caa aat acc atc aca gga cta agc aac act cta gct aat gtt acc aat 3744
 Gln Asn Thr Ile Thr Gly Leu Ser Asn Thr Leu Ala Asn Val Thr Asn
 1235 1240 1245

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FIG.4N

gat aaa ggt agc gta cgc acc aca gaa cag ggc aat ata atc aaa gac 3792
 Asp Lys Gly Ser Val Arg Thr Thr Glu Gln Gly Asn Ile Ile Lys Asp
 1250 1255 1260

gaa gac aaa acc cgt gcc gcc agc att gtt gat gtg cta agc gca ggc 3840
 Glu Asp Lys Thr Arg Ala Ala Ser Ile Val Asp Val Leu Ser Ala Gly
 1265 1270 1275 1280

ttt aac ttg caa ggc aat ggt gaa gog gtt gac ttt gtc toc act tat 3888
 Phe Asn Leu Gln Gly Asn Gly Glu Ala Val Asp Phe Val Ser Thr Tyr
 1285 1290 1295

gac acc gtc aac ttt gcc aat ggc aat acc acc acc gct aag gtg acc 3936
 Asp Thr Val Asn Phe Ala Asn Gly Asn Thr Thr Thr Ala Lys Val Thr
 1300 1305 1310

tat gat gac aca agc aaa acc agt aaa gtg gtc tat gat gtc aat gtg 3984
 Tyr Asp Asp Thr Ser Lys Thr Ser Lys Val Val Tyr Asp Val Asn Val
 1315 1320 1325

gat gat aca acc att gaa gtt aaa gat aaa aaa ctt ggc gta aaa acc 4032
 Asp Asp Thr Thr Ile Glu Val Lys Asp Lys Lys Leu Gly Val Lys Thr
 1330 1335 1340

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FIG.40

acc aca ttg acc agt act ggc aca ggt gct aat aaa ttt gcc cta agc 4080
 Thr Thr Leu Thr Ser Thr Gly Thr Gly Ala Asn Lys Phe Ala Leu Ser
 1345 1350 1355 1360
 aat caa gct act ggc gat gcg ctt gtc aag gcc agt gat atc gtt gct 4128
 Asn Gln Ala Thr Gly Asp Ala Leu Val Lys Ala Ser Asp Ile Val Ala
 1365 1370 1375
 cat cta aac acc tta tct ggc gac atc caa act gcc aaa ggg gca agc 4176
 His Leu Asn Thr Leu Ser Gly Asp Ile Gln Thr Ala Lys Gly Ala Ser
 1380 1385 1390
 caa gcg aac aac tca gca ggc tat gtg gat gct gat ggc aat aag gtc 4224
 Gln Ala Asn Asn Ser Ala Gly Tyr Val Asp Ala Asp Gly Asn Lys Val
 1395 1400 1405
 atc tat gac agt acc gat aac aag tac tat caa gcc aaa aat gat ggc 4272
 Ile Tyr Asp Ser Thr Asp Asn Lys Tyr Tyr Gln Ala Lys Asn Asp Gly
 1410 1415 1420
 aca gtt gat aaa acc aaa gaa gtt gcc aaa gac aaa ctg gtc gcc caa 4320
 Thr Val Asp Lys Thr Lys Glu Val Ala Lys Asp Lys Leu Val Ala Gln
 1425 1430 1435 1440

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FIG.4P

gcc caa acc cca gat ggc aca ttg gct caa atg aat gtc aaa tca gtc 4368
 Ala Gln Thr Pro Asp Gly Thr Leu Ala Gln Met Asn Val Lys Ser Val 1445
 1445

att aac aaa gaa caa gta aat gat gcc aat aaa aag caa ggc atc aat 4416
 Ile Asn Lys Glu Gln Val Asn Asp Ala Asn Lys Lys Gln Gly Ile Asn 1460
 1460

gaa gac aac gcc ttt gtt aaa gga ctt gaa aaa gcc gct tct gat aac 4464
 Glu Asp Asn Ala Phe Val Lys Gly Leu Glu Lys Ala Ala Ser Asp Asn 1475
 1475

aaa acc aaa aac gcc gca gta act gtg ggt gat tta aat gcc gtt gcc 4512
 Lys Thr Lys Asn Ala Ala Val Thr Val Gly Asp Leu Asn Ala Val Ala 1490
 1490

caa aca cog ctg acc ttt gca ggg gat aca ggc aca acg gct aaa aaa 4560
 Gln Thr Pro Leu Thr Phe Ala Gly Asp Thr Gly Thr Thr Ala Lys Lys 1505
 1505

ctg ggc gag act ttg acc atc aaa ggt ggg caa aca gac acc aat aag 4608
 Leu Gly Glu Thr Leu Thr Ile Lys Gly Gly Gln Thr Asp Thr Asn Lys 1525
 1525

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FIG.4Q

cta acc gat aat aac atc ggt gtg gta gca ggt act gat ggc ttc act	4656
Leu Thr Asp Asn Asn Ile Gly Val Val Ala Gly Thr Asp Gly Phe Thr	1540 1545 1550
gtc aaa ctt gcc aaa gac cta acc aat ctt aac agc gtt aat gca ggt	4704
Val Lys Leu Ala Lys Asp Leu Thr Asn Leu Asn Ser Val Asn Ala Gly	1555 1560 1565
ggc acc aaa att gat gaa aaa ggc atc tct ttt gta gac gca aac ggt	4752
Gly Thr Lys Ile Asp Glu Lys Gly Ile Ser Phe Val Asp Ala Asn Gly	1570 1575 1580
caa gcc aaa gca aac acc cct gtg cta agt gcc aat ggg ctg gac ctg	4800
Gln Ala Lys Ala Asn Thr Pro Val Leu Ser Ala Asn Gly Leu Asp Leu	1585 1590 1595 1600
ggt ggc aag gtc atc agt aat gtg ggc aaa ggc aca aaa gat acc gac	4848
Gly Gly Lys Val Ile Ser Asn Val Gly Lys Gly Thr Lys Asp Thr Asp	1605 1610 1615
gct gcc aat gta caa cag tta aac gaa gta cgc aac ttg ttg ggt ctt	4896
Ala Ala Asn Val Gln Gln Leu Asn Glu Val Arg Asn Leu Leu Gly Leu	1620 1625 1630

FIG.4R

ggt aat gat aac gct gac ggc aat cag gta aac att gcc gac atc aaa 4944
 Gly Asn Asp Asn Ala Asp Gly Asn Gln Val Asn Ile Ala Asp Ile Lys
 1635 1640 1645

aaa gac cca aat tca ggt tca tca tct aac cgc act gtc atc aaa gca 4992
 Lys Asp Pro Asn Ser Gly Ser Ser Ser Asn Arg Thr Val Ile Lys Ala
 1650 1655 1660

ggc acg gta ctt ggc ggt aaa ggt aat aac gat acc gaa aaa ctt gcc 5040
 Gly Thr Val Leu Gly Gly Lys Gly Asn Asn Asp Thr Glu Lys Leu Ala
 1665 1670 1675 1680

act ggt ggt gta caa gtg ggc gtg gat aaa gac ggc aac gct aac ggc 5088
 Thr Gly Gly Val Gln Val Gly Val Asp Lys Asp Gly Asn Ala Asn Gly
 1685 1690 1695

gat tta agc aat gtt tgg gtc aaa acc caa aaa gat ggc agc aaa aaa 5136
 Asp Leu Ser Asn Val Trp Val Lys Thr Gln Lys Lys Asp Gly Ser Lys Lys
 1700 1705 1710

gcc ctg ctc gcc act tat aac gcc gca ggt cag acc aac tat gtg acc 5184
 Ala Leu Leu Ala Thr Tyr Asn Ala Ala Gly Gln Thr Asn Tyr Val Thr
 1715 1720 1725

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FIG.4S

aac aac ccc gca gaa gcc att gac aga ata aat gaa caa ggt atc ogc 5232
 Asn Asn Pro Ala Glu Ala Ile Asp Arg Ile Asn Glu Gln Gly Ile Arg
 1730 1735 1740

 ttc ttc cat gtc aac gat ggc aat caa gag cct gtg gta caa ggg ogc 5280
 Phe Phe His Val Asn Asp Gly Asn Gln Glu Pro Val Val Gln Gly Arg
 1745 1750 1755 1760

 aac ggc att gac tca agt gcc tca ggc aag cac tca gtg gog ata ggt 5328
 Asn Gly Ile Asp Ser Ser Ala Ser Gly Lys His Ser Val Ala Ile Gly
 1765 1770 1775

 ttc cag gcc aag gca gat ggt gaa gcc gcc gtt gcc ata ggc aga caa 5376
 Phe Gln Ala Lys Ala Asp Gly Glu Ala Ala Val Ala Ile Gly Arg Gln
 1780 1785 1790

 acc caa gca ggc aac caa tcc atc gcc atc ggt gat aac gca caa gcc 5424
 Thr Gln Ala Gly Asn Gln Ser Ile Ala Ile Gly Asp Asn Ala Gln Ala
 1795 1800 1805

 acg ggc gat caa tcc atc gcc atc ggt aca ggc aat gtg gta gca ggt 5472
 Thr Gly Asp Gln Ser Ile Ala Ile Gly Thr Gly Asn Val Val Ala Gly
 1810 1815 1820

FIG.4T

aag cac tct ggt gcc atc ggc gac cca agc act gtt aag gct gat aac 5520
 Lys His Ser Gly Ala Ile Gly Asp Pro Ser Thr Val Lys Ala Asp Asn
 1825 1830 1835 1840
 agt tac agt gtg ggt aat aac aac cag ttt acc gat gcc act caa acc 5568
 Ser Tyr Ser Val Gly Asn Asn Asn Gln Phe Thr Asp Ala Thr Gln Thr
 1845 1850 1855
 gat gtc ttt ggt gtg ggc aat aac atc acc atc gtc acc gaa agt aac tog 5616
 Asp Val Phe Gly Val Gly Asn Asn Ile Thr Val Thr Glu Ser Asn Ser
 1860 1865 1870
 gtt gcc tta ggt tca aac tct gcc atc agt gca ggc aca cac gca ggc 5664
 Val Ala Leu Gly Ser Asn Ser Ala Ile Ser Ala Gly Thr His Ala Gly
 1875 1880 1885
 aca caa gcc aaa tct gac ggc aca gca ggt aca acc acc aca gca 5712
 Thr Gln Ala Lys Lys Ser Asp Gly Thr Ala Gly Thr Thr Thr Ala
 1890 1895 1900
 ggt gcc aca ggt acg gtt aaa ggc ttt gct gga caa acg gcg gtt ggt 5760
 Gly Ala Thr Gly Thr Val Lys Gly Phe Ala Gly Gln Thr Ala Val Gly
 1905 1910 1915 1920

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FIG.4U

gog gtc tcc gtg ggt gcc tca ggt gct gaa cgc cgt atc caa aat gtg Ala Val Ser Val Gly Ala Ser Gly Ala Glu Arg Arg Ile Gln Asn Val 1925 1930 1935	5808
gca gca ggt gag gtc agt gcc acc agc acc gat gog gtc aat ggt agc Ala Ala Gly Glu Val Ser Ala Thr Ser Thr Asp Ala Val Asn Gly Ser 1940 1945 1950	5856
cag ttg tac aaa gcc acc caa agc att gcc aac gca acc aat gag ctt Gln Leu Tyr Lys Ala Thr Gln Ser Ile Ala Asn Ala Thr Asn Glu Leu 1955 1960 1965	5904
gac cat cgt atc cac caa aac gaa aat aaa gcc aat gca ggg att tca Asp His Arg Ile His Gln Asn Glu Asn Lys Ala Asn Ala Gly Ile Ser 1970 1975 1980	5952
tca gog atg gog atg gog tcc atg cca caa gcc tac att cct ggc aga Ser Ala Met Ala Met Ala Ser Met Pro Gln Ala Tyr Ile Pro Gly Arg 1985 1990 1995 2000	6000
tcc atg gtt acc ggg ggt att gcc acc cac aac ggt caa ggt gog gtg Ser Met Val Thr Gly Gly Ile Ala Thr His Asn Gly Gln Gly Ala Val 2005 2010 2015	6048

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FIG.4V

gca gtg gga ctg tog aag ctg tog gat aat ggt caa tgg gta ttt aaa	6096
Ala Val Gly Leu Ser Lys Leu Ser Asp Asn Gly Gln Trp Val Phe Lys	
2020	2030
atc aat ggt tca gcc gat acc caa ggc cat gta ggg gog gca gtt ggt	6144
Ile Asn Gly Ser Ala Asp Thr Gln Gly His Val Gly Ala Ala Val Gly	
2035	2045
gca ggt ttt cac ttt	6159
Ala Gly Phe His Phe	
2050	

FIG.5A

Moraxella catarrhalis les1 200kDa

ATG aat cac atc tat aaa gtc atc ttt aac aaa gcc aca ggc aca ttt 48
 Met Asn His Ile Tyr Lys Val Ile Phe Asn Lys Ala Thr Gly Thr Phe 15
 1 5 10

atg gcc gtg gca gag tgc gcc aaa tcc cac agc gga ggg agt agc agt 96
 Met Ala Val Ala Glu Cys Ala Lys Ser His Ser Gly Gly Ser Ser Ser 30
 20 25

agt acc gca gga cag gtg ggc agc tct cct gtc atc cgc ctg act cgt 144
 Ser Thr Ala Gly Gln Val Gly Ser Ser Pro Val Ile Arg Leu Thr Arg 45
 35 40

gtt gcc acg ctc gct atc cta gtg atc ggt gog acg ctc aat ggc agt 192
 Val Ala Thr Leu Ala Ile Leu Val Ile Gly Ala Thr Leu Asn Gly Ser 60
 50 55

gct tat gct caa aat aat agc aag atc gca ttt ggt acc aca ggc aac 240
 Ala Tyr Ala Gln Asn Asn Ser Lys Ile Ala Phe Gly Thr Thr Gly Asn 75
 65 70 80

aat gac aat gcc tog gct agc aat gaa gca tcc att gct att ggt agt 288
 Asn Asp Asn Ala Ser Ala Ser Asn Glu Ala Ser Ile Ala Ile Gly Ser 90
 85 95

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FIG.5B

ctt gct aag gca cat gcc aat caa gct att gct atc ggt ggt agc aaa 336
 Leu Ala Lys Ala His Ala Asn Gln Ala Ile Ala Ile Gly Gly Ser Lys
 100 105 110

cca gat cct cgt aat caa gcg gct aat cag aag gca ggt tcc cac gcc 384
 Pro Asp Pro Arg Asn Gln Ala Ala Asn Gln Lys Ala Gly Ser His Ala
 115 120 125

aaa ggt aaa gag tcc atc gcc atc ggt gat gta ctg gct gag ggt 432
 Lys Gly Lys Glu Ser Ile Ala Ile Gly Gly Asp Val Leu Ala Glu Gly
 130 135 140

gat gcc tcg att gcc att ggt agt gat gac tta tat ttg gat agg aat 480
 Asp Ala Ser Ile Ala Ile Gly Ser Asp Asp Leu Tyr Leu Asp Arg Asn
 145 150 155 160

agc act aac tct aaa tat cca aat ggt ctt ctt agc act ctt att caa 528
 Ser Thr Asn Ser Lys Tyr Pro Asn Gly Leu Leu Ser Thr Leu Ile Gln
 165 170 175

aac cat aca gta tta ogc caa ata cga gac tca aat ggt tct cag aaa 576
 Asn His Thr Val Leu Arg Gln Ile Arg Asp Ser Asn Gly Ser Gln Lys
 180 185 190

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FIG.5C

tat aga cgc aca gca gca gaa gga cac gcc agt act gca gtg gga gcc	624
Tyr Arg Arg Thr Ala Ala Glu Gly His Ala Ser Thr Ala Val Gly Ala	
195 200 205	
atg gca tat gca aag ggt cat ttt gcc aac gcc ttt ggt aca cgg tca	672
Met Ala Tyr Ala Lys Gly His Phe Ala Asn Ala Phe Gly Thr Arg Ser	
210 215 220	
aca gct gaa ggc aac tat tcc ttg gca gta ggt ctt acc gcc aaa gcc	720
Thr Ala Glu Gly Asn Tyr Ser Leu Ala Val Gly Leu Thr Ala Lys Ala	
225 230 235 240	
gaa aaa gga tat aca atc gct att ggt tct aat gca caa gct atc aat	768
Glu Lys Gly Tyr Thr Ile Ala Ile Gly Ser Asn Ala Gln Ala Ile Asn	
245 250 255	
tat gga gca cta gcc ctt ggt gca gat act cga gtt gat ttg gat tac	816
Tyr Gly Ala Leu Ala Leu Gly Ala Asp Thr Arg Val Asp Leu Asp Tyr	
260 265 270	
ggt att gcc cta ggt tat ggt tct cag atc ctt aat aat aat aat	864
Gly Ile Ala Leu Gly Tyr Gly Ser Gln Ile Leu Asn Asn Asn Asn	
275 280 285	

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FIG.5D

aat aat aat aaa gcc tat gta cca gaa ggt aat ggg tca aac ata aaa 912
 Asn Asn Asn Lys Ala Tyr Val Pro Glu Gly Asn Gly Ser Asn Ile Lys
 290 295 300

tog tct aaa gcc acc ggc aat ggt tta ttt tcc att ggt agt agc act 960
 Ser Ser Lys Ala Thr Gly Asn Gly Leu Phe Ser Ile Gly Ser Ser Thr
 305 310 315 320

atc aag cgt aaa atc atc aat gtc ggt gca ggt tat gag gat acc gat 1008
 Ile Lys Arg Lys Ile Ile Asn Val Gly Ala Gly Tyr Glu Asp Thr Asp
 325 330 335

gcg gtc aat gtg gca cag cta aaa gcg gtg gag aat ctg gct aag cgt 1056
 Ala Val Asn Val Ala Gln Leu Lys Ala Val Glu Asn Leu Ala Lys Arg
 340 345 350

caa att act ttt aag ggt gat gat aac ggt act ggc gtt aag aaa aaa 1104
 Gln Ile Thr Phe Lys Lys Gly Asp Asp Asn Gly Thr Gly Val Lys Lys Lys
 355 360 365

ctg ggc gag act tta acc att aaa ggt ggt gag acc caa gcg gac aag 1152
 Leu Gly Glu Thr Leu Thr Ile Lys Lys Gly Gly Glu Thr Gln Ala Asp Lys
 370 375 380

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FIG.5E

cta acc gat aat aac att ggt gtg gta aca gat aat aat act ggt	1200
Leu Thr Asp Asn Asn Ile Gly Val Val Thr Asp Asn Asn Thr Gly	
385 390 395 400	
ctg aaa gtt aaa ctt gct aaa aac cta agc ggt ctt gaa aca gtt agc	1248
Leu Lys Val Lys Leu Ala Lys Asn Leu Ser Gly Leu Glu Thr Val Ser	
405 410 415	
acc aaa aac cta acc gcc agc gag aaa gtt acg gta ggt agt ggt aat	1296
Thr Lys Asn Leu Thr Ala Ser Glu Lys Val Thr Val Gly Ser Gly Asn	
420 425 430	
aac acc gct gag cta caa agc ggt ggt tta acc ttt acc cca aca aca	1344
Asn Thr Ala Glu Leu Gln Ser Gly Gly Leu Thr Phe Thr Pro Thr Thr	
435 440 445	
aat gca agc aca gac aaa acc gtc tat ggc act gat ggg ctt aag ttt	1392
Asn Ala Ser Thr Asp Lys Thr Val Tyr Gly Thr Asp Gly Leu Lys Phe	
450 455 460	
act gat aat tct aat acg gca ctt gaa gat act act cgt atc acc aaa	1440
Thr Asp Asn Ser Asn Thr Ala Leu Glu Asp Thr Thr Arg Ile Thr Lys	
465 470 475 480	

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FIG.5F

gat aaa att ggt ttt agc aat aaa gct ggt aca gtt gat gaa aac aaa Asp Lys Ile Gly Phe Ser Asn Lys Ala Gly Thr Val Asp Glu Asn Lys	1488
485 490 495	
cct tat ctt gat aaa gac aag cta aaa gtt ggc aac agc acc cta aac Pro Tyr Leu Asp Lys Asp Lys Leu Lys Val Gly Asn Ser Thr Leu Asn	1536
500 505 510	
aac ggt ggc ttg act gtt aat aac acc att ggt ggt agc aat aaa caa Asn Gly Gly Leu Thr Val Asn Asn Thr Ile Gly Gly Ser Asn Lys Gln	1584
515 520 525	
atc caa gtc ggt gct gat ggc att aaa ttt gcc gat gtg aat gtt aat Ile Gln Val Gly Ala Asp Gly Ile Lys Phe Ala Asp Val Asn Val Asn	1632
530 535 540	
gta tca aat gcc gca aaa ttc ggc act act act cgt att acc gaa gag gaa Val Ser Asn Ala Ala Lys Phe Gly Thr Thr Arg Ile Thr Glu Glu Glu	1680
545 550 555 560	
att ggc ttt gct gat gct gat ggt aaa gtt gat aaa aag tca cca tat Ile Gly Phe Ala Asp Ala Asp Gly Lys Val Asp Lys Lys Ser Pro Tyr	1728
565 570 575	

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FIG.5G

ttg gat aaa caa ctt caa gtg ggt ggt gtt aaa att acc aaa gac	1776
Leu Asp Lys Lys Gln Leu Gln Val Gly Gly Val Lys Ile Thr Lys Asp	
580 585 590	
agt ggc att aat gca ggt gat caa aag atc agt aat gtt aaa gat gca	1824
Ser Gly Ile Asn Ala Gly Asp Gln Lys Ile Ser Asn Val Lys Asp Ala	
595 600 605	
aog gac gat acc gat gca gtc act tat aaa cag ctt aaa caa gtc caa	1872
Thr Asp Asp Thr Asp Ala Val Thr Tyr Lys Lys Gln Leu Lys Gln Val Gln	
610 615 620	
caa gac gcc gac ggt gcc cta caa agc ttc tct att cgt gat gaa aaa	1920
Gln Asp Ala Asp Gly Ala Leu Gln Ser Phe Ser Ile Arg Asp Glu Lys	
625 630 635 640	
ggt cag gaa ttt acg att agt aac ttg tat tct aat ggt aat acc cca	1968
Gly Gln Glu Phe Thr Ile Ser Asn Leu Tyr Ser Asn Gly Asn Thr Pro	
645 650 655	
aat acc ttt gag acc atc acc ttt gca ggt gaa aac ggc atc agt atc	2016
Asn Thr Phe Glu Thr Ile Thr Phe Ala Gly Glu Asn Gly Ile Ser Ile	
660 665 670	

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FIG.5H

agc aat gac ata gcc aaa ggt aaa gtc aaa gtt ggt att gac cca atc Ser Asn Asp Ile Ala Lys Gly Lys Val Lys Val Gly Ile Asp Pro Ile 675 680 685	2064
aat ggt ctc aoc acg cct aag ctg acc gtg ggt agc gat aaa gat ggt Asn Gly Leu Thr Thr Pro Lys Leu Thr Val Gly Ser Asp Lys Asp Gly 690 695 700	2112
aaa act caa ttg gtt att gag caa gtg gct agc ggt aac gac acc aaa Lys Thr Gln Leu Val Ile Glu Gln Val Ala Ser Gly Asn Asp Thr Lys 705 710 715 720	2160
aac atc att aga gga ttg tcc cca aca ctg cct agc att acc aat gca Asn Ile Ile Arg Gly Leu Ser Pro Thr Leu Pro Ser Ile Thr Asn Ala 725 730 735	2208
ggt ggc gta cgc acc aca gaa cag ggc aat aca atc acc agc gac gaa Gly Gly Val Arg Thr Thr Glu Gln Gly Asn Thr Ile Thr Ser Asp Glu 740 745 750	2256
gac aaa tcc aaa gcc gcc agt atc ggt gat ata tta aat aca ggc ttt Asp Lys Ser Lys Ala Ala Ser Ile Gly Asp Ile Leu Asn Thr Gly Phe 755 760 765	2304

FIG. 5I

aac cta aaa aat aat agc aac tcc gtt ggc ttt gtc tcc act tat aac 2352
 Asn Leu Lys Asn Asn Ser Asn Ser Val Gly Phe Val Ser Thr Tyr Asn
 770 775 780
 act gtt gac ttt atc gat ggc aat gcc acc acc gct aag gta act tac 2400
 Thr Val Asp Phe Ile Asp Gly Asn Ala Thr Thr Ala Lys Val Thr Tyr
 785 790 795 800
 gat gaa acc aat caa acc agt aaa gta act tat gat gtc aat gtg gat 2448
 Asp Glu Thr Asn Gln Thr Ser Lys Val Thr Tyr Asp Val Asn Val Asp
 805 810 815
 gag aaa acc att gaa ctc aca ggc gat aat ggc aag aca aac aaa att 2496
 Glu Lys Thr Ile Glu Leu Thr Gly Asp Asn Gly Lys Thr Asn Lys Ile
 820 825 830
 ggc gtc aaa acc acc aca ctg acc aca aca aat gct aat ggt aaa gca 2544
 Gly Val Lys Thr Thr Thr Leu Thr Thr Thr Asn Ala Asn Gly Lys Ala
 835 840 845
 acc aac ttt agt acc acc gat aac gat gcc ctt gtt aac gcc aaa gac 2592
 Thr Asn Phe Ser Thr Thr Asp Asn Asp Ala Leu Val Asn Ala Lys Asp
 850 855 860

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FIG.5J

atc gcc gaa aat cta aac acc cta gcc aag gaa att cac acc acc aaa 2640
 Ile Ala Glu Asn Leu Asn Thr Leu Ala Lys Glu Ile His Thr Thr Lys
 865 870 875 880

ggc aca goa gac acc gcc cta caa acc ttt aaa gtc aaa aac gac ggt 2688
 Gly Thr Ala Asp Thr Ala Leu Gln Thr Phe Lys Val Lys Lys Asp Gly
 885 890 895

gca act gat gac gaa acc atc acc gtg ggt aaa gat ggt aca caa aac 2736
 Ala Thr Asp Asp Glu Thr Ile Thr Val Gly Lys Asp Gly Thr Gln Asn
 900 905 910

ggc aag acc gtc aac act cta aaa ctc aaa ggt gaa aac ggt cta acg 2784
 Gly Lys Thr Val Asn Thr Leu Lys Leu Lys Gly Glu Asn Gly Leu Thr
 915 920 925

gtt gct acc aat aaa gat ggt acg gtt acc ttt ggc att aac acc caa 2832
 Val Ala Thr Asn Lys Asp Gly Thr Val Thr Phe Gly Ile Asn Thr Gln
 930 935 940

agc ggt ctt aaa gcc ggc gac agc acc act cta aac aaa gat ggc ttg 2880
 Ser Gly Leu Lys Ala Gly Asp Ser Thr Thr Leu Asn Lys Asp Gly Leu
 945 950 955 960

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FIG.5K

tct att aaa aac ccc gct agt aac gaa caa atc caa gtc ggt gct gat Ser Ile Lys Asn Pro Ala Ser Asn Glu Gln Ile Gln Val Gly Ala Asp	965 970 975	2928
ggc gtg aag ttt gcc aag gtt gat aag ggt aat tca agc act ggc att Gly Val Lys Phe Ala Lys Val Asp Lys Gly Asn Ser Ser Thr Gly Ile	980 985 990	2976
gat ggc aca agc cgt atc acc aaa gat caa att ggc ttt act ggg gct Asp Gly Thr Ser Arg Ile Thr Lys Asp Gln Ile Gly Phe Thr Gly Ala	995 1000 1005	3024
aat ggc tca ctt gat acc acc aaa ccc cac cta acc aaa gac aag ctt Asn Gly Ser Leu Asp Thr Thr Lys Pro His Leu Thr Lys Asp Lys Leu	1010 1015 1020	3072
aaa gtg ggt gaa gtt gaa att acc aac act ggc att aac gca ggt ggt Lys Val Gly Glu Val Glu Ile Thr Asn Thr Gly Ile Asn Ala Gly Gly	1025 1030 1035 1040	3120
aaa aag att acc aac att caa tca ggt gat att acc caa aac agc aat Lys Lys Ile Thr Asn Ile Gln Ser Gly Asp Ile Thr Gln Asn Ser Asn	1045 1050 1055	3168

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FIG.5L

gat gct gtg aca ggc ggt ogg gtt tat gat tta aaa acc gaa ctt gaa Asp Ala Val Thr Gly Gly Arg Val Tyr Asp Leu Lys Thr Glu Leu Glu	1060 1065 1070	3216
agc aaa atc aac agt gct gct gct aaa aca gca caa aac tca tta cac gaa Ser Lys Ile Asn Ser Ala Ala Lys Thr Ala Gln Asn Ser Leu His Glu	1075 1080 1085	3264
ttc tca gta gca gat gaa caa ggt aat cac ttt aog gtt agt aac cct Phe Ser Val Ala Asp Glu Gln Gly Asn His Phe Thr Val Ser Asn Pro	1090 1095 1100	3312
tac tcc agt tat gac acc tca aag acc tct gat gtc atc acc ttt gca Tyr Ser Ser Tyr Asp Thr Ser Lys Thr Ser Asp Val Ile Thr Phe Ala	1105 1110 1115 1120	3360
ggc gaa aac ggc att acc acc aag gta aat aaa ggt gtg cgt gtg Gly Glu Asn Gly Ile Thr Thr Lys Val Asn Lys Lys Gly Val Arg Val	1125 1130 1135	3408
ggc att gac caa acc aaa ggc tta acc aog cct aag ctg acc gtg ggt Gly Ile Asp Gln Thr Lys Gly Leu Thr Thr Pro Lys Leu Thr Val Gly	1140 1145 1150	3456

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FIG.5M

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aat aat aat ggc aaa ggc att gtc att gac agt aaa gat ggt caa aat      3504
Asn Asn Asn Gly Lys Gly Ile Val Ile Asp Ser Lys Asp Gly Gln Asn
1155      1160      1165

aac atc aca gga cta agc aac act cta gct aat gtt acc aat gat ggt      3552
Thr Ile Thr Gly Leu Ser Asn Thr Leu Ala Asn Val Thr Asn Asp Gly
1170      1175      1180

gca gga cac gca cta agc caa ggg ctt gcc aat gac acc gac aaa acc      3600
Ala Gly His Ala Leu Ser Gln Gly Leu Ala Asn Asp Thr Asp Lys Thr
1185      1190      1195      1200

cgt gcc gcc agc att ggt gat gtg cta aac gca ggc ttt aac ttg caa      3648
Arg Ala Ala Ser Ile Gly Asp Val Leu Asn Ala Gly Phe Asn Leu Gln
1205      1210      1215

ggc aat ggt gaa gcg gtt gac ttt gtc tcc act tat gac act gtt gac      3696
Gly Asn Gly Glu Ala Val Asp Phe Val Ser Thr Tyr Asp Thr Val Asp
1220      1225      1230

ttt atc gat ggc aat gcc acc acc gct aag gtg acc tat gat gac aca      3744
Phe Ile Asp Gly Asn Ala Thr Thr Ala Lys Val Thr Tyr Asp Asp Thr
1235      1240      1245

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FIG.5N

agc aaa acc agt aaa gtg gtc tat gat gtc aat gtg gat aat aaa acc 3792
 Ser Lys Thr Ser Lys Val Val Tyr Asp Val Asn Val Asp Asn Lys Thr
 1250 1255 1260

att gaa gtg aca agt gat aaa aaa ctt ggc gtc aaa acc acc aca ctg 3840
 Ile Glu Val Thr Ser Asp Lys Lys Leu Gly Val Lys Thr Thr Thr Leu
 1265 1270 1275 1280

acc aaa aca agt gct aat ggt aat gca acc aaa ttt agt gcc gcc gat 3888
 Thr Lys Thr Ser Ala Asn Gly Asn Ala Thr Lys Phe Ser Ala Ala Asp
 1285 1290 1295

ggc gat gcc ctt gtt aaa gcc agt gat atc gcc acc cat cta aat acc 3936
 Gly Asp Ala Leu Val Lys Ala Ser Asp Ile Ala Thr His Leu Asn Thr
 1300 1305 1310

ttg gct ggc gac atc caa acc gcc aaa ggc gca agc caa gca agc agc 3984
 Leu Ala Gly Asp Ile Gln Thr Ala Lys Lys Gly Ala Ser Gln Ala Ser Ser
 1315 1320 1325

tca gca agc tat gtg gat gct gat ggc aac aag gtc atc tat gac agt 4032
 Ser Ala Ser Tyr Val Asp Ala Asp Gly Asn Lys Val Ile Tyr Asp Ser
 1330 1335 1340

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FIG.50

acc gat aag aag tac tat caa gtc aat gac aag ggt caa gtg gac aaa 4080
 Thr Asp Lys Lys Tyr Tyr Gln Val Asn Asp Lys Gly Gln Val Asp Lys
 1345 1350 1355 1360
 aac aaa gaa gtt gcc aaa gac aaa ctg gtc gcc caa gcc caa acc cca 4128
 Asn Lys Glu Val Ala Lys Asp Lys Leu Val Ala Gln Ala Gln Thr Pro
 1365 1370 1375
 gat ggc aca ttg gct caa atg aat gtc aaa toa gtc att aac aaa gag 4176
 Asp Gly Thr Leu Ala Gln Met Asn Val Lys Ser Val Ile Asn Lys Glu
 1380 1385 1390
 caa gta aat gat gcc aat aaa aag caa ggc atc aat gaa gac aac gcc 4224
 Gln Val Asn Asp Ala Asn Lys Lys Gln Gly Ile Asn Glu Asp Asn Ala
 1395 1400 1405
 ttt atc aaa ggg ctt gaa aac gcc gcc aaa gac acc aaa acc aaa aac 4272
 Phe Ile Lys Gly Leu Glu Asn Ala Ala Lys Asp Thr Lys Thr Lys Asn
 1410 1415 1420
 gcc gca gta act gtg ggt gat tta aat gcc gtt gcc caa aca cag ctg 4320
 Ala Ala Val Thr Val Gly Asp Leu Asn Ala Val Ala Gln Thr Pro Leu
 1425 1430 1435 1440

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FIG.5P

acc ttt gca ggg gat aca ggc aca acg gct aaa aaa ctg ggc gag act 4368
 Thr Phe Ala Gly Asp Thr Gly Thr Thr Ala Lys Lys Leu Gly Glu Thr 1445
 1445
 ttg acc atc aaa ggt ggg caa aca gac acc aat aag cta acc gat aat 4416
 Leu Thr Ile Lys Gly Gly Gln Thr Thr Asp Thr Asn Lys Leu Thr Asp Asn 1460
 1460
 aac atc ggt gtg gta gca ggt act gat ggc ttc act gtc aaa ctt gcc 4464
 Asn Ile Gly Val Val Ala Gly Thr Asp Gly Phe Thr Val Lys Leu Ala 1475
 1475
 aaa gac cta acc aat ctt aac agc gtt aat gca ggt ggc acc aga att 4512
 Lys Asp Leu Thr Asn Leu Asn Ser Val Asn Ala Gly Gly Thr Arg Ile 1490
 1490
 gat gaa aaa ggc atc tct ttt gta gac gca aac ggt caa gcc aaa gca 4560
 Asp Glu Lys Gly Ile Ser Phe Val Asp Ala Asn Gly Gln Ala Lys Ala 1505
 1505
 aac acc cct gtg cta agt gcc aat ggg ctg gac ctg ggt ggc aaa cgc 4608
 Asn Thr Pro Val Leu Ser Ala Asn Gly Leu Asp Leu Gly Gly Lys Arg 1525
 1525

FIG.5Q

atc agt aac atc ggt gca gct gtt gat gat aac gat gog gtg aac ttt 4656
 Ile Ser Asn Ile Gly Ala Ala Val Asp Asp Asn Asp Ala Val Asn Phe
 1540 1545 1550
 aag cag ttt aat gaa gtt gcc aaa acg gtc aac aac cta aac aac caa 4704
 Lys Gln Phe Asn Glu Val Ala Lys Thr Val Asn Asn Leu Asn Asn Gln
 1555 1560 1565
 agt aac tca ggt gog tca tta ccc ttt gtg gta acc gat gcc aat ggc 4752
 Ser Asn Ser Gly Ala Ser Leu Pro Phe Val Val Thr Asp Ala Asn Gly
 1570 1575 1580
 aag ccc atc aat ggc acc gat ggc aag ccc caa aaa gcc atc aag ggc 4800
 Lys Pro Ile Asn Gly Thr Asp Gly Lys Pro Gln Lys Ala Ile Lys Gly
 1585 1590 1595 1600
 gcc gat ggt aaa tac tat cac gcc aac gcc aac ggc gta cct gtg gac 4848
 Ala Asp Gly Lys Tyr Tyr His Ala Asn Ala Asn Gly Val Pro Val Asp
 1605 1610 1615
 aaa gat ggc aag ccc atc acc gat gog gac aaa ctt gcc aat ctg gca 4896
 Lys Asp Gly Lys Pro Ile Thr Asp Ala Asp Lys Leu Ala Asn Leu Ala
 1620 1625 1630

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FIG.5R

gct cat ggc aaa ccc ctt gat gca ggt cat caa gtg gtg gca agc cta Ala His Gly Lys Pro Leu Asp Ala Gly His Gln Val Val Ala Ser Leu 1635 1640 1645	4944
ggc ggc aac tca gat gcc atc acc cta acc aac atc aag tcc act ttg Gly Gly Asn Ser Asp Ala Ile Thr Leu Thr Asn Ile Lys Ser Thr Leu 1650 1655 1660	4992
cca caa att gac aca cca aac aca ggt aat gcc aat gca ggg caa gcc Pro Gln Ile Asp Thr Pro Asn Thr Gly Asn Ala Asn Ala Gly Gln Ala 1665 1670 1675 1680	5040
caa agt ctg ccc agc cta tca gca gca cag caa agt aat gct gcc agt Gln Ser Leu Pro Ser Leu Ser Ala Ala Gln Gln Ser Asn Ala Ala Ser 1685 1690 1695	5088
gtc aaa gat gtg cta aat gta ggc ttt aac ttg cag acc aat cac aat Val Lys Asp Val Leu Asn Val Gly Phe Asn Leu Gln Thr Asn His Asn 1700 1705 1710	5136
caa gtg gac ttt gtc aaa gcc tat gat acc gtc aac ttt gtc aat ggt Gln Val Asp Phe Val Lys Ala Tyr Asp Thr Val Asn Phe Val Asn Gly 1715 1720 1725	5184

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FIG.5S

aca ggt gcc gac atc aca agc gtg cgt agt gct gat ggc acg atg agt	5232
Thr Gly Ala Asp Ile Thr Ser Val Arg Ser Ala Asp Gly Thr Met Ser	
1730 1735 1740	
aac atc acc gtc aac acc gcc tta gca gcg acc gat gat gat ggc aat	5280
Asn Ile Thr Val Asn Thr Ala Leu Ala Thr Asp Asp Asp Gly Asn	
1745 1750 1755 1760	
gtg ctt atc aaa gcc aaa gat ggt aag ttc tac aaa gca gac gac ctc	5328
Val Leu Ile Lys Ala Lys Asp Gly Lys Phe Tyr Lys Ala Asp Asp Leu	
1765 1770 1775	
atg cca aac ggc tca cta aaa gca ggc aaa tca gcc agt gat gcc aaa	5376
Met Pro Asn Gly Ser Leu Lys Ala Gly Lys Ser Ala Ser Asp Ala Lys	
1780 1785 1790	
act cca act ggt cta agc ctt gtt aac ccc aat gct ggt aaa ggc agt	5424
Thr Pro Thr Gly Leu Ser Leu Val Asn Pro Asn Ala Gly Lys Gly Ser	
1795 1800 1805	
aca ggc gat gca gtg gct ctt aat aac tta tca aaa gog gta ttt aaa	5472
Thr Gly Asp Ala Val Ala Leu Asn Asn Leu Ser Lys Ala Val Phe Lys	
1810 1815 1820	

FIG.5T

toc aaa gat ggt aca act act acc aca gta agc tct gat ggc atc agt 5520
 Ser Lys Asp Gly Thr Thr Thr Thr Val Ser Ser Asp Gly Ile Ser
 1825 1830 1835 1840
 atc caa ggc aaa gat aac agc agc atc acc cta agc aaa gat ggg ctg 5568
 Ile Gln Gly Lys Asp Asn Ser Ser Ile Thr Leu Ser Lys Asp Gly Leu
 1845 1850 1855
 aat gta ggc ggt aag gtc atc agc aat gtg ggt aaa ggc aca aaa gac 5616
 Asn Val Gly Gly Lys Val Ile Ser Asn Val Gly Lys Gly Thr Lys Asp
 1860 1865 1870
 acc gac gct gcc aat gta caa cag tta aac gaa gta cgc aac ttg ttg 5664
 Thr Asp Ala Ala Asn Val Gln Gln Leu Asn Glu Val Arg Asn Leu Leu
 1875 1880 1885
 ggt ctt ggt aat gct ggt aat gat aac gct gac ggc aat cag gta aac 5712
 Gly Leu Gly Asn Ala Gly Asn Asp Asn Ala Asp Gly Asn Gln Val Asn
 1890 1895 1900
 att gcc gac atc aaa gac cca aat tca ggt tca tct aac cgc 5760
 Ile Ala Asp Ile Lys Lys Asp Pro Asn Ser Gly Ser Ser Ser Asn Arg
 1905 1910 1915 1920

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FIG.5U

act gtc atc aaa gca ggc acg gta ctt ggc ggt aaa ggt aat aac gat 5808
 Thr Val Ile Lys Ala Gly Thr Val Leu Gly Gly Lys Gly Asn Asn Asp 1925 1930 1935

acc gaa aaa ctt gcc act ggt ggt gta caa gtg ggc gtg gat aaa gac 5856
 Thr Glu Lys Lys Leu Ala Thr Gly Gly Val Gln Val Gly Val Asp Lys Asp 1940 1945 1950

ggc aac gct aac ggc gat tta agc aat gtt tgg gtc aaa acc caa aaa 5904
 Gly Asn Ala Asn Gly Asp Leu Ser Asn Val Trp Val Lys Thr Gln Lys 1955 1960 1965

gat ggc agc aaa aaa gcc ctg ctc gcc act tat aac gcc gca ggt cag 5952
 Asp Gly Ser Lys Lys Ala Leu Leu Ala Thr Tyr Asn Ala Ala Gly Gln 1970 1975 1980

acc aac tat ttg acc aac aac ccc gca gaa gcc att gac aga ata aat 6000
 Thr Asn Tyr Leu Thr Asn Asn Pro Ala Glu Ala Ile Asp Arg Ile Asn 1985 1990 1995 2000

gaa caa ggt atc cgc ttc cat gtc aac gat ggc aat caa gag cct 6048
 Glu Gln Gly Ile Arg Phe Phe His Val Asn Asp Gly Asn Gln Glu Pro 2005 2010 2015

FIG.5V

gtg gta caa ggg cgt aac ggc att gac tca agt gcc tca ggc aag cac 6096
 Val Val Gln Gly Arg Asn Gly Ile Asp Ser Ser Ala Ser Gly Lys His
 2020 2025 2030
 tca gtg gcg ata ggt ttc cag gcc aag gca gat ggt gaa gcc gcc gtt 6144
 Ser Val Ala Ile Gly Phe Gln Ala Lys Ala Asp Gly Glu Ala Ala Val
 2035 2040 2045
 gcc ata ggc aga caa acc caa gca ggc aac caa tcc atc gcc atc ggt 6192
 Ala Ile Gly Arg Gln Thr Gln Ala Gly Asn Gln Ser Ile Ala Ile Gly
 2050 2055 2060
 gat aac gca caa gcc acg ggc gat caa tcc atc gcc atc ggt aca ggc 6240
 Asp Asn Ala Gln Ala Thr Gly Asp Gln Ser Ile Ala Ile Gly Thr Gly
 2065 2070 2075 2080
 aat gtg gta aca ggt aag cac tct ggt gcc atc ggc gac cca agc act 6288
 Asn Val Val Thr Gly Lys His Ser Gly Ala Ile Gly Asp Pro Ser Thr
 2085 2090 2095
 gtt aag gct gat aac agt tac agt gtg ggt aat aac aac cag ttt atc 6336
 Val Lys Ala Asp Asn Ser Tyr Ser Val Gly Asn Asn Asn Gln Phe Ile
 2100 2105 2110

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FIG.5W

gat gcc act cag acc gat gtc ttt ggt gtg ggc aat aac atc acc gtg 6384
 Asp Ala Thr Gln Thr Asp Val Phe Gly Val Gly Asn Asn Ile Thr Val
 2115 2120 2125

 acc gaa agt aac tog gtt gcc tta ggt tca aac tct gcc atc agt gca 6432
 Thr Glu Ser Asn Ser Val Ala Leu Gly Ser Asn Ser Ala Ile Ser Ala
 2130 2135 2140

 ggc aca cac gca ggc aca caa gcc aaa aaa tct gac ggc aca gca ggt 6480
 Gly Thr His Ala Gly Thr Gln Ala Lys Lys Ser Asp Gly Thr Ala Gly
 2145 2150 2155 2160

 aca acc acc aca gca ggt gca aca ggt acg gtt aaa ggc ttt gct gga 6528
 Thr Thr Thr Ala Gly Ala Thr Gly Thr Val Lys Gly Phe Ala Gly
 2165 2170 2175

 caa acg gcg gtt ggt gcg gtc tcc gtg ggt gcc tca ggt gct gaa cgc 6576
 Gln Thr Ala Val Gly Ala Val Ser Val Gly Ala Ser Gly Ala Glu Arg
 2180 2185 2190

 cgt atc caa aat gtg gca gca ggt gag gtc agt gcc acc agc acc gat 6624
 Arg Ile Gln Asn Val Ala Ala Gly Glu Val Ser Ala Thr Ser Thr Asp
 2195 2200 2205

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FIG.5X

gog gtc aat ggt agc cag ttg tac aaa gcc acc caa ggc att gcc aac Ala Val Asn Gly Ser Gln Leu Tyr Lys Ala Thr Gln Gly Ile Ala Asn 2210 2215 2220	6672
gca acc aat gag ctt gac cat ogt atc cac caa aac gaa aat aaa gcc Ala Thr Asn Glu Leu Asp His Arg Ile His Gln Asn Glu Asn Lys Ala 2225 2230 2235 2240	6720
aat gca ggg att tca tca gog atg gog atg gog tcc atg cca caa gcc Asn Ala Gly Ile Ser Ser Ala Met Ala Met Ala Ser Met Pro Gln Ala 2245 2250 2255	6768
tac att cct ggc aga tcc atg gtt acc ggg ggt att gcc acc cac aac Tyr Ile Pro Gly Arg Ser Met Val Thr Gly Gly Ile Ala Thr His Asn 2260 2265 2270	6816
ggt caa ggt gog gtg gca gtg gga ctg tog aag ctg tog gat aat ggt Gly Gln Gly Ala Val Ala Val Gly Leu Ser Lys Leu Ser Asp Asn Gly 2275 2280 2285	6864
caa tgg gta ttt aaa atc aat ggt tca gcc gat acc caa ggc cat gta Gln Trp Val Phe Lys Ile Asn Gly Ser Ala Asp Thr Gln Gly His Val 2290 2295 2300	6912

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6942

FIG.5Y

ggg gcg gca gtt ggt gca ggt ttt cac ttt
Gly Ala Ala Val Gly Ala Gly Phe His Phe
2305 2310

FIG. 6A

Alignment of amino acid sequence of 200kDa proteins of *M. catarrhalis* strains

10 20 30 40 50 60 ...
 MNHIVKVFNKATGTFMVAEYAKSHSTGGSCATGQVGSVCTLSFARIAALAVLVIGATLSGS...
R.....N.....
C.....G.SS.STA.....SPVIRLT.V.T.I.....N.....
 ... 70 80 90 100
 ...AYAQQKDTKHIAIGEONQPRRS--GTAKADGDRAIAIG 4223
QIT..-E..QT.KINNVILK.D.L.T.EAS..F. Q8
NNSK--..F.TTGNDNA-----S.SNEAS..... LES-1

 110 120 130 140 150 160 ...
 ENANAQGGQAIAGSSNKTVNGSSLD-KIGTDATQESIAIGDVKASGDASIAIGSDDIHLID...
 SLSK...S.....VKPDP.NG.NG-NV.SH.K.N.....L.E.....Y.PK...
 SL.K.HAN.....G.KPDPNRQANQ.A.SH.K.K.....L.E.....Y.DR...
 ... 170 180 190 200
 ...QHGNPKHPKGTLLINDLINGHAVLKEIRSSKNDNVKYR 4223
 ...NLDL-.NEEFHK-----H..EI..K.QT.T.GKI... Q8
 ...NST.S.Y.N.L.ST-..QN.T..RQ..D.NGSQ-.... LES-1

 210 220 230 240 250 260 ...
 PRTTASGHASTAVGAMSYAQGHFSNAFGTRATAKSAYSIAVGLAATAEGQSTIAIGSDATSSSLG...
 ...R.Q.....Y..EA.....Q.TK..S..V..N.KANAF...
 ...A.E.....A..K..A.....S..EGN.....T.K..KGY.....N.QAINY....

FIG.6B

... 270 280 290 300
 ...AIALGAGTRAQLGSSIALGQGSVVTSQDNN-SRPAYT 4223
 ...T.I.GN.VVN.GRGV...F..QILDR...TDAS..V Q8
 ...L....D..VD.DYG...Y..QIILNN..NNK..V LES-1

310 320 330 340 350 ...
 PNIQALDPKFQ--ATNNKAGPL-SIG-SN-----SIKRKIINVGAGVAKTDAVNVAQLEAVWKW...
 .LGKT.ADQYK--..RQGDSTDIF...N..NNNS..R.....SRD.....KL.EEL...
 .EEGNSNIKSS-K..----GNG.F...-----SST.....YED.....K..ENL...
 ... 360 370 380 390 400
 ...AKERRITFQGD-IN-STDVKIGLDNLTIKGGAETNA--LTDNN-IGVV 4223
-N.K...K..G..N.NS.ER..G.....D.Q....-..EA.-... Q8
-Q...K...-G.G..KK.GE.....-Q.DK.....N.... LES-1

410 420 430 440 450 460 ...
 KEADNSGLKVKI AKTIANNL TEVNPTIINATTTVKVGSSTTAEILLSDSLFTIQPNIGSQSTSK...
 TDCN--.....E.TG..S.-----S..NKIT.SNINNN..Q.GG...S-.I..TK-.D....
 TDNN-T.....N.SG.ET.S.KN.T.SEK.T...GNN-.....Q.GG....-T.NA-.D....
 ... 470 480 490 500
 ...TVYGANGVKFINNAETTAIGITRITRDKIGFARDG 4223
SID.L....DSNSI.TK.....KK.....GTN Q8
TD.L....D.SN.ALED-.....K.....SNKA LES-1

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FIG.6C

```

D-----...
.GVDESKPYLDNEKLVGNSTLNSGSLTVNNT--TCNKQIQVGANGIKFATVANNVANISATVG...
GTVDENKPYLDKDKLVGNSTLNNGLTVNNTIGGSNKQIQVGADGIKFADVNVNVSN-AAKFG...
...510520530
...-----VDEKQAPYLDKKQLKVGSVAITIDNGIDA4223
...TARUTEEKIGFAGINDG...-ER...R.E..T.S..N.Q8
...TTRUTEEEIGFADADCK..-KS.....Q..G.K..K.S..N.LES-1

540550560570580590...
GNKKISNLA KGSSANDAVTIEQLKAAPTINAGAGISVTPTEISVDAKSGNVTAPTINIGVKTT...
..H..TG..TN..IANT...K..D.....D...INSNNGDLVDS...I.T.....S.....
.DQ....VKDATDDT...YK...-----...
...600
...ELNSDG
...K...N.
...-----

610620630640650660...
TSD--KFSVKGSGTNNSLVTAEHLASVINEVARTADSALQSFVKEEDDDANAITVAKDTTKN...
..GNN...SNAHD.....KD..D...K..E.....P..K.K.QNG-.NSN.....G...--.....
-----Q.QOD..G.....SIRD.-KGQEFT.SNLYSNGNT...

```

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FIG.6D

... 670 680 690 700
 ...AGAVSILKLGKNGELTVATKD-GIVTFGLSQDSGLTIG 4223
 ...GKTFNT...E..VNIT.NRAT.....ID.SN...TP Q8
 ...PNTFETITFA.E..ISISNDIAK.K.KV.IDPIN...TP LES-1

710 720 730 740 750 ...
 KST-----LNDGLTVKDTNEQIQV--GANGIKFTNWGSPGIGIANTARITRDKIGFA...
 .L.VGSDTN-----NR-LV-I..VP-SADG.ST.NLIK-----...
 .L.VGSDKD-----K.QLV-I..VASG---DT.NIIR-----...
 ... 760 770 780 790 800
 ...GSDGAVDTNKPYLDDQDKLVGNVKITNIGINAGGKAITGLSPTLPSI 4223
 ...-----... Q8
 ...-----... LES-1

810 820 830 840 850 860 ...
 ADQSS-RNIELGNTIQ-DKDKSNAASINDIINTGFNLKNNNPIDFVSTVDIVDFANGNATTAT...
 .SP.G-...A....E-E.....D.V.A.....GDK.....T...ID.....
 TNAGGV.TT.Q....TS.E...K....G.....S.SVG.....NT...ID.....K...

FIG.6E

...	870	880	890	900	
...VTHDTANKTSKVVDVNVDDTTHLITGTDNKK---					4223
...Y.E..Q....A.....EK..E...--..G.KQ-.....					Q8
...Y.ET.Q....T.....EK..E...--..G.TNKI.....					LES-1

910	920	930	940	950	960	...
TKLNKTSANGTAINFNVNSSDED-ALVNAKDIAENLNTLAKEIHTTKGTADTALQTFIVKKVD...						
I..TE..T...-..T...-..T.D.H...K.S...G.....E.....N.....						
.T.TT.N...K-.....-STT.N.-.....K....-..						

...	970	980	990	1000	
...ENNADDDANALTVGQKNANQ--VNLTILKGENGLNIKT					4223
...DK...T.....KDGTSK--...K...K...D...					Q8
...--DG.T.DET....KGTQ.GKT....K.....TVA.					LES-1

1010	1020	1030	1040	1050	1060	...
DKNGTVTFGINVTSGLKAGKST-LNDGGLSIKPTGSEQIQGADGVKFAKVNNGVVGAGIDG...						
..D.....Q.....D..T..NN.....TASN.....M.....						
N.D.....Q.....D..T..KD.....ASN.....DK-.NSST.....						

...	1070	1080	1090	1100	
...TTRITRDEIGFTGINGSLDKSKPHLSKDGINAGGKI-----					4223
.....S...K.Q.....A.....TT....T..KLKV.EVE.TNIGINAGGKI					Q8
.....S...K.Q.....A.....TT....T..KLKV.EVE.TNIGINAGGKI					LES-1

FIG.6F

1110 1120 1130 1140 1150 1160 ...
TNIQSGELAQNSHDAVTGGKIYDLKTELENKISSAKTAQNSLHEFSVADEQGNFIVSNPYSS...
K.....
D.T...N.....RV.....S.N.A.....H.....
... 1170 1180 1190 1200
...YDTSKTSDVITFAGENGITTKVANKGWRVIGIDQIKG
.....
.....

4223
Q8
LES-1

1210 1220 1230 1240 1250 1260 ...
LITPKLTVGNNGKIVIDSQNGQNTTIGLSNTLANVINDKGSVRITTEQGNIIKDEDKTRAASI...
N.....
KD.....AGHALS...LAN-.T.....
... 1270 1280 1290 1300
...VDVLSAGFNLQNGEAVDFVSTYDITVNEADGNATTA
.....N..T...
...G...N.....D.I.....

4223
Q8
LES-1

FIG.6G

1310 1320 1330 1340 1350 1360 ...
 KVTYDDTSKTSKVYDVNVDDTTIEVK-DKKLGVKITTLTSTGTGANKFALSNOATGDALVKAS...

NK.....TS.....K.SANG.ATKF.A-.D.....
 ... 1370 1380 1390 1400
 ...DIVAHLNTLSGDIQTAKGASQANNISAGYVDADGNKVI

AT.....A.....SS..S.....

4223
 Q8
 LES-1

1410 1420 1430 1440 1450 1460 ...
 YDSTDNKYYQAKNDGTVDKTKEVAKDKLVAAQAQTPDGTILAQNNKSVINKEQVNDANKKQGINE...

K....VNDK.Q...N.....
 ... 1470 1480 1490 1500
 ...DNAFVKGLEKKAASDNKTNAAVTVGDINAVAQTPILT

I...N.K.T.....

4223
 Q8
 LES-1

FIG.6H

1510 1520 1530 1540 1550 1560 ...
FAGDIGTTAKKLGELTIKGGQIDINKLITNNIGWAGIDGFIVKLAKDLTNLNSVNAAGTKID...
.....
.....
... 1570 1580 1590
...DKGVSEFVDSGQAKANTPVL SANGIDL~-----
...E..I...AN.....
...E..I...AN.....GGKRI

4223
Q8
LES-1

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SNIGAAVDNDNAVNFQFNEVAKTVNNLNNQNSGASLPIFVITDANGKPTINGTDGKPKQKAIKGA...
...-----
...-----
...DKGYHANANGVPVDKDGKPIITDADKLANLAHGKP

4223
Q8
LES-1

LDAGHQVWASLGGNSDAITLTNIKSTLPQIDTPTNTGNAGQAQSLPSLSAAQQSNVAAVKDVL...

FIG. 61

4223
Q8
LES-1

.....
.....
.....
..... NVGENLQTNHNOVDFVKAYDTNFFVANGICADITSVR

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4223
Q8
LES-1

SADGIMSNITVTALAAATDDDGENVLIKAKDGFYKADDLMFNGSLKAGKSASDAKTPTGLSLVN...
 ...
 PNAGKGSTGDVAVALNNLSKAVFKSKDGTITTTTVSSD
 ...

1600

GGKVISNVG

-----GANSIANG
-----,.....
GISIQKUNSSITLSKDGLNV.....
.....
.....
.....

4223
Q8
LES-1

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FIG.6J

1610	1620	1630	1640	1650	1660	...
KGTKDTDAANVQQINIEVRNLLGLGNAGNDNADGNQVNIADIKKDPNSGSSSNRTVTKAGTVLGG...						
.....						
.....						
...	1670	1680	1690	1700		
...KGNNDTEKLATGGIQVGVDKDGNAVNGDLSNWMVKIQ						
.....V.....						
.....V.....						

4223
Q8
LES-1

1710	1720	1730	1740	1750	1760	...
KDGSKKALLATYNAGQINYLITNNPAEIDRINEQGIREFHNDGNQEPVWQGRNGIDSSASCK...						
.....V.....						
.....						
...	1770	1780	1790	1800		
...HSVAIGFQAKADGEFAVAIGRQIQAGNQSIAGINA						
.....						
.....						

4223
Q8
LES-1

FIG.6K

1810 1820 1830 1840 1850 1860 ...
QATGDSIAIGTCNVAGKHSGAIGDPSTVKADNSYSVGNNOFTDATQTDVFGVGNITVIES...
.....
.....T.....
.....I.....
... 1870 1880 1890 1900
...NSVALGSNSAISAGTHAGTQAKKSDGTAGTTTAGA
.....
.....
.....

4223
Q8
LES-1

1910 1920 1930 1940 1950 1960 ...
TGTVKGFAGQTAVGAVSVGASCAERRIQNVAAGEVSVSATSTDAVNGSQLYKATQSIANATNELDH...
.....
.....G.....
... 1970 1980 1990 2000
...RIHQENKANAGISSAMAMASMPQAYIPGRSMVTGG
.....
.....

4223
Q8
LES-1

FIG.6L

2010	2020	2030	2040
IATHNQGAVAVGLSKLSDNQWFKINGSADTQGHVGAAVGAGHFH*			
.....*			
.....*			
.....	...		
.....	...		
.....	...		

4223
Q8
LES-1

...
...
...

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Construction of Plasmids Expressing Portions of the 200 kDa Protein Gene from Strain 4223

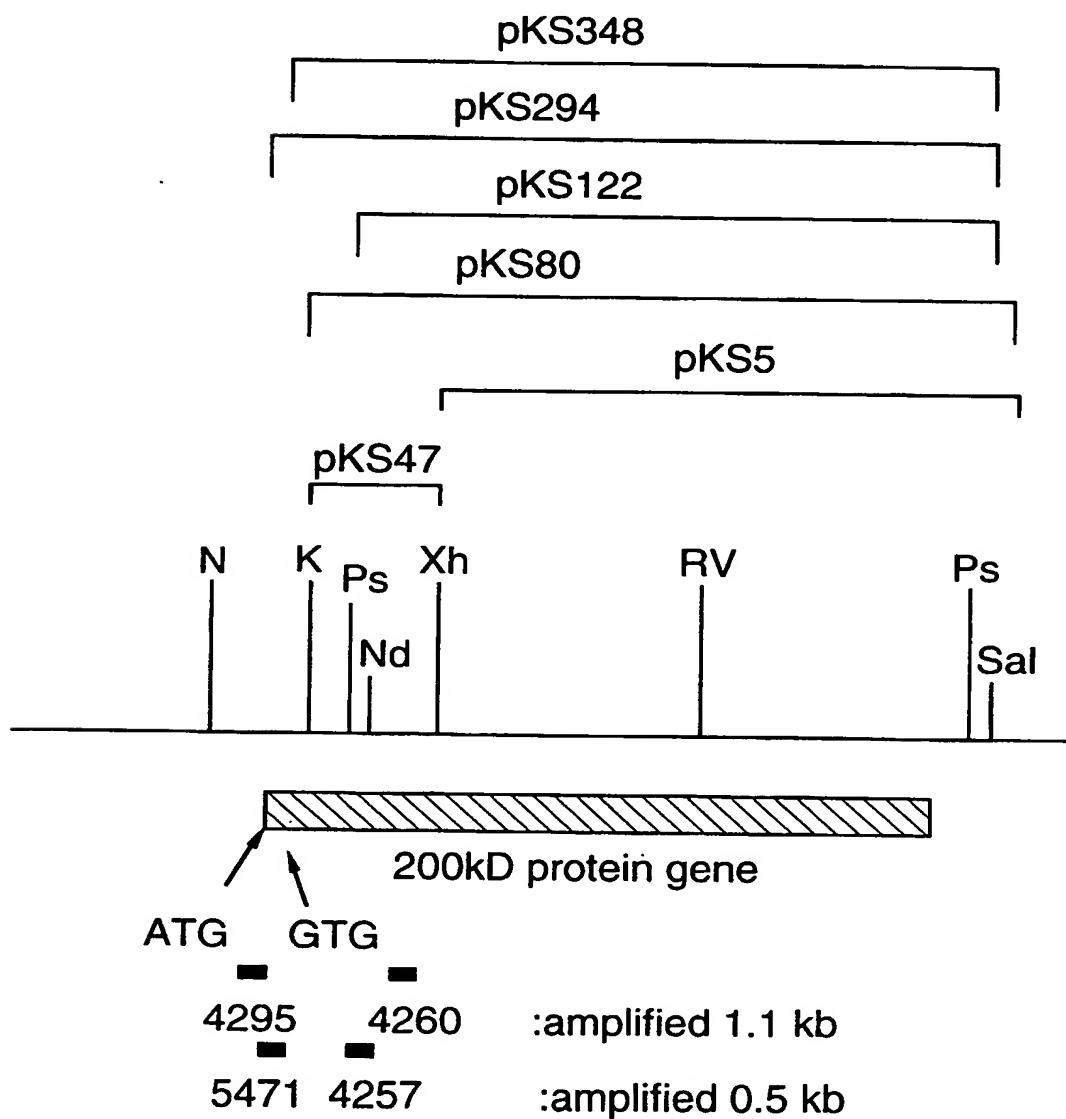


FIG.7

FIG.8A

M. catarrhalis M56 200kDa gene in pKS348.

ATG atc ggt gca acg ctc agt ggc agt gct tat gct caa aaa aaa gat 48
 Met Ile Gly Ala Thr Leu Ser Gly Ser Ala Tyr Ala Gln Lys Lys Asp 15
 1 5 10 15
 acc aaa cat atc gca att ggt gaa caa aac cag cca aga cgc tca ggc 96
 Thr Lys His Ile Ala Ile Gly Glu Gln Asn Gln Pro Arg Arg Ser Gly 30
 20 25 30
 act gcc aag gcg gac ggt gat cga gcc att gct att ggt gaa aat gct 144
 Thr Ala Lys Ala Asp Gly Asp Arg Ala Ile Ala Ile Gly Glu Asn Ala 45
 35 40 45
 aac gca cag ggc ggt caa gcc atc gcc atc ggt agt agt aat aaa act 192
 Asn Ala Gln Gly Gly Gln Ala Ile Ala Ile Gly Ser Ser Asn Lys Thr 60
 50 55 60
 gtc aat gga agc agt ttg gat aag ata ggt acc gat gct acg ggt caa 240
 Val Asn Gly Ser Ser Leu Asp Lys Ile Gly Thr Asp Ala Thr Gly Gln 75
 65 70 80

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FIG.8B

gag tcc atc gcc atc ggt ggt gat gta aag gct agt ggt gat gcc tog 288
 Glu Ser Ile Ala Ile Gly Gly Asp Val Lys Ala Ser Gly Asp Ala Ser 95
 85 90

att gcc atc ggt agt gat gac tta cat ttg ctt gat cag cat ggt aat 336
 Ile Ala Ile Gly Ser Asp Asp Leu His Leu Leu Asp Gln His Gly Asn 110
 100 105

cct aaa cat cag aaa ggt act ctg att aac gat ctt att aac ggc cat 384
 Pro Lys His Pro Lys Gly Thr Leu Ile Asn Asp Leu Ile Asn Gly His 125
 115 120

gca gta tta aaa gaa ata cga agc tca aag gat aat gat gta aaa tat 432
 Ala Val Leu Lys Glu Ile Arg Ser Ser Lys Asp Asn Asp Val Lys Tyr 140
 130 135

aga cgc aca acc gca agc gga cac gcc agt act gca gtg gga gcc atg 480
 Arg Arg Thr Thr Ala Ser Gly His Ala Ser Thr Ala Val Gly Ala Met 160
 145 150 155

tca tat gca cag ggt cat ttt toc aac gcc ttt ggt aca cgg gca aca 528
 Ser Tyr Ala Gln Gly His Phe Ser Asn Ala Phe Gly Thr Arg Ala Thr 175
 165 170

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FIG.8C

gct aaa agt gcc tat tcc ttg gca gtg ggt ctt gcc gcc aca gcc gag 576
 Ala Lys Ser Ala Tyr Ser Leu Ala Val Gly Leu Ala Ala Thr Ala Glu
 180 185 190

gcc caa tct aca atc gct att ggt tct gat gca aca tct agc tog ttg 624
 Gly Gln Ser Thr Ile Ala Ile Gly Ser Asp Ala Thr Ser Ser Ser Leu
 195 200 205

gga gog ata gcc ctt ggt gca ggt act cgt gct cag cta cag ggc agt 672
 Gly Ala Ile Ala Leu Gly Ala Gly Thr Arg Ala Gln Leu Gln Gly Ser
 210 215 220

att gcc cta ggt caa ggt tct gtt gtc act cag agt gat aat aat tct 720
 Ile Ala Leu Gly Gln Gly Ser Val Thr Thr Gln Ser Asp Asn Asn Ser
 225 230 235 240

aga cag gcc tat aca cca aat acc cag gca cta gac ccc aag ttt caa 768
 Arg Pro Ala Tyr Thr Pro Asn Thr Gln Ala Leu Asp Pro Lys Phe Gln
 245 250 255

gcc acc aat aat aag aag gog ggt cca ctt toc att ggt agt aac tct 816
 Ala Thr Asn Asn Thr Lys Ala Gly Pro Leu Ser Ile Gly Ser Asn Ser
 260 265 270

FIG.8D

atc aaa cgt aaa atc atc atc gtc ggt gca ggt gtt aat aaa acc gat 864
 Ile Lys Arg Lys Ile Ile Asn Val Gly Ala Gly Val Asn Lys Thr Asp 285
 275

gcg gtc aat gtg gca cag cta gaa gcg gtg aag tgg gct aag gag 912
 Ala Val Asn Val Ala Gln Leu Glu Ala Val Lys Trp Ala Lys Glu 300
 290

cgt aga att act ttt cag ggt gat gat aac agt act gac gta aaa ata 960
 Arg Arg Ile Thr Phe Gln Gly Asp Asn Ser Thr Asp Val Lys Ile 315
 305

ggt ttg gat aat act tta act att aaa ggt ggt gca gag acc aac gca 1008
 Gly Leu Asp Asn Thr Leu Thr Ile Lys Gly Gly Ala Glu Thr Asn Ala 330
 325

tta acc gat aat aat atc ggt gtg gta aaa gag gct gat aat agt ggt 1056
 Leu Thr Asp Asn Asn Ile Gly Val Val Lys Glu Ala Asp Asn Ser Gly 345
 340

ctg aaa gtt aaa ctt gct aaa act tta aac aat ctt act gag gtg aat 1104
 Leu Lys Val Lys Leu Ala Lys Thr Leu Asn Asn Leu Thr Glu Val Asn 360
 355

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FIG.8E

aca act aca tta aat gcc aca acc aca gtt aag gta ggt agt agt agt	1152
Thr Thr Thr Leu Asn Ala Thr Thr Thr Val Lys Val Gly Ser Ser Ser	
370 375 380	
agt act aca gct gaa tta ttg agt gat agt tta acc ttt acc cag ccc	1200
Ser Thr Thr Ala Glu Leu Leu Ser Asp Ser Leu Thr Phe Thr Gln Pro	
385 390 395 400	
aat aca ggc agt caa agc aca agc aaa acc gtc tat ggc gtt aat ggg	1248
Asn Thr Gly Ser Gln Ser Thr Ser Lys Thr Val Tyr Gly Val Asn Gly	
405 410 415	
gtg aag ttt act aat aat gca gaa aca aca gca atc ggc act act	1296
Val Lys Phe Thr Asn Asn Ala Glu Thr Thr Ala Ala Ile Gly Thr Thr	
420 425 430	
cgt att acc aga gat aaa att ggc ttt gct oga gat ggt gat gtt gat	1344
Arg Ile Thr Arg Asp Lys Ile Gly Phe Ala Arg Asp Gly Asp Val Asp	
435 440 445	
gaa aaa caa gca cca tat ttg gat aaa aaa caa ctt aaa gtg ggt agt	1392
Glu Lys Gln Ala Pro Tyr Leu Asp Lys Lys Gln Leu Lys Val Gly Ser	
450 455 460	

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FIG.8F

gtt gca att acc ata gac aat ggc att gat gca ggt aat aaa aag atc	1440
Val Ala Ile Thr Ile Asp Asn Gly Ile Asp Ala Gly Asn Lys Lys Ile	
465 470 475 480	
agt aat ctt gcc aaa ggt agc agt gct aac gat gcg gtt acc atc gaa	1488
Ser Asn Leu Ala Lys Gly Ser Ser Ala Asn Asp Ala Val Thr Ile Glu	
485 490 495	
cag ctc aaa gcc gcc aag cct act tta aac gca ggc gct ggc atc agt	1536
Gln Leu Lys Ala Ala Lys Pro Thr Leu Asn Ala Gly Ala Gly Ile Ser	
500 505 510	
gtc aca cct act gaa ata tca gtt gat gct aag agt ggc aat gtt acc	1584
Val Thr Pro Thr Glu Ile Ser Val Asp Ala Lys Ser Gly Asn Val Thr	
515 520 525	
gcc cca act tac aac att ggc gtg aaa acc acc gag ctt aac agt gat	1632
Ala Pro Thr Tyr Asn Ile Gly Val Lys Thr Thr Glu Leu Asn Ser Asp	
530 535 540	
ggc act agt gat aaa ttt agt gtt aag ggt agt ggt acg aac aat agc	1680
Gly Thr Ser Asp Lys Phe Ser Val Lys Gly Ser Gly Thr Asn Asn Ser	
545 550 555 560	

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FIG.8G

tta gtt acc gcc gaa cat ttg gca agc tat cta aat gaa gtc aat oga	1728
Leu Val Thr Ala Glu His Leu Ala Ser Tyr Leu Asn Glu Val Asn Arg	
565 570 575	
acg gct gac agt gct cta caa agc ttt acc gtt aaa gaa gaa gac gat	1776
Thr Ala Asp Ser Ala Leu Gln Ser Phe Thr Val Lys Glu Glu Asp Asp	
580 585 590	
gat gac gcc aac gct atc acc gtg gct aaa gat acg aca aaa aat gcc	1824
Asp Asp Ala Asn Ala Ile Thr Val Ala Lys Asp Thr Thr Lys Asn Ala	
595 600 605	
ggc gca gtc agc atc tta aaa ctc aaa ggt aaa aac ggt cta acg gtt	1872
Gly Ala Val Ser Ile Leu Lys Leu Lys Gly Lys Asn Gly Leu Thr Val	
610 615 620	
gct acc aaa aaa gat ggt acg gtt acc ttt ggg ctt agc caa gat agc	1920
Ala Thr Lys Lys Asp Gly Thr Val Thr Phe Gly Leu Ser Gln Asp Ser	
625 630 635 640	
ggt ctg acc att ggc aaa agc acc cta aac aac gat ggc ttg act gtt	1968
Gly Leu Thr Ile Gly Lys Ser Thr Leu Asn Asn Asp Gly Leu Thr Val	
645 650 655	

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FIG.8H

aaa gat acc aac gaa caa atc caa gtc ggt gct aat ggc att aaa ttt Lys Asp Thr Asn Glu Gln Ile Gln Val Gly Ala Asn Gly Ile Lys Phe	2016
660 665 670	
act aat gtg aat ggt agt aat cca ggt act ggc att gca aat acc gct Thr Asn Val Asn Gly Ser Asn Pro Gly Thr Gly Ile Ala Asn Thr Ala	2064
675 680 685	
ogc att acc aga gat aaa att ggc ttt gct ggt tct gat ggt gca gtt Arg Ile Thr Arg Asp Lys Ile Gly Phe Ala Gly Ser Asp Gly Ala Val	2112
690 695 700	
gat aca aac aaa cct tat ctt gat caa gac aag cta caa gtt ggc aat Asp Thr Asn Lys Pro Tyr Leu Asp Gln Asp Lys Leu Gln Val Gly Asn	2160
705 710 715 720	
gtt aag att acc aac act ggc att aac gca ggt ggt aaa gcc atc aca Val Lys Ile Thr Asn Thr Gly Ile Asn Ala Gly Gly Lys Ala Ile Thr	2208
725 730 735	
ggg ctg tcc cca aca ctg cct agc att gcc gat caa agt agc ogc aac Gly Leu Ser Pro Thr Leu Pro Ser Ile Ala Asp Gln Ser Ser Arg Asn	2256
740 745 750	

FIG.8I

ata gaa ctg ggc aat aca atc caa gac aaa gac aaa tcc aac gct gcc 2304
 Ile Glu Leu Gly Asn Thr Ile Gln Asp Lys Asp Lys Ser Asn Ala Ala
 755 760 765
 agc att aat gat ata tta aat aca ggc ttt aac cta aaa aat aat aac 2352
 Ser Ile Asn Asp Ile Leu Asn Thr Gly Phe Asn Leu Lys Asn Asn Asn
 770 775 780
 aac ccc att gac ttt gtc tcc act tat gac att gtt gac ttt gcc aat 2400
 Asn Pro Ile Asp Phe Val Ser Thr Tyr Asp Ile Val Asp Phe Ala Asn
 785 790 795 800
 ggc aat gcc acc acc gcc aca gta acc cat gat acc gct aac aaa acc 2448
 Gly Asn Ala Thr Thr Ala Thr Val Thr His Asp Thr Ala Asn Lys Thr
 805 810 815
 agt aaa gtg gta tat gat gtg aat gtg gat gat aca acc att cat cta 2496
 Ser Lys Val Val Tyr Asp Val Asn Val Asp Asp Thr Thr Ile His Leu
 820 825 830
 aca ggc act gat gac aat aaa aaa ctt ggc gtc aaa acc acc aaa ctg 2544
 Thr Gly Thr Asp Asp Asn Lys Lys Leu Gly Val Lys Thr Thr Lys Leu
 835 840 845

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FIG.8J

aac aaa aca agt gct aat ggt aat aca gca act aac ttt aat gtt aac 2592
 Asn Lys Thr Ser Ala Asn Gly Asn Thr Ala Thr Asn Phe Asn Val Asn
 850 855 860

tct agt gat gaa gat gcc ctt gtt aac gcc aaa gac atc gcc gaa aat 2640
 Ser Ser Asp Glu Asp Ala Leu Val Asn Ala Lys Asp Ile Ala Glu Asn
 865 870 875 880

cta aac acc cta gcc aag gaa att cac acc acc aaa ggc aca gca gac 2688
 Leu Asn Thr Leu Ala Lys Glu Ile His Thr Thr Lys Gly Thr Ala Asp
 885 890 895

acc gcc cta caa acc ttt acc gtt aaa aag gta gat gaa aat aat aat 2736
 Thr Ala Leu Gln Thr Phe Thr Val Lys Lys Val Asp Glu Asn Asn Asn
 900 905 910

gct gat gac gcc aac gcc atc acc gtg ggt caa aag aac gca aat aat 2784
 Ala Asp Asp Ala Asn Ala Ile Thr Val Gly Gln Lys Asn Ala Asn Asn
 915 920 925

caa gtc aac acc cta aca ctc aaa ggt gaa aac ggt ctt aat att aaa 2832
 Gln Val Asn Thr Leu Thr Lys Lys Gly Glu Asn Gly Leu Asn Ile Lys
 930 935 940

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FIG.8K

acc gac aaa aat ggt acg gtt acc ttt ggc att aac acc aca agc ggt 2880
 Thr Asp Lys Asn Gly Thr Val Thr Phe Gly Ile Asn Thr Thr Ser Gly
 945 950 955 960
 ctt aaa gcc ggc aaa agc acc cta aac gac ggt ggc ttg tct att aaa 2928
 Leu Lys Ala Gly Lys Ser Thr Leu Asn Asp Gly Gly Leu Ser Ile Lys
 965 970 975
 aac ccc act ggt agc gaa caa atc caa gtc ggt gct gat ggc gtg aag 2976
 Asn Pro Thr Gly Ser Glu Gln Ile Gln Val Gly Ala Asp Gly Val Lys
 980 985 990
 ttt gcc aag gtt aat aat ggt gtt gta ggt gct ggc att gat ggc 3024
 Phe Ala Lys Val Asn Asn Gly Val Val Gly Ala Gly Ile Asp Gly
 995 1000 1005
 aca act cgc att acc aga gat gaa att ggc ttt act ggc act aat ggc 3072
 Thr Thr Arg Ile Thr Arg Asp Glu Ile Gly Phe Thr Gly Thr Asn Gly
 1010 1015 1020
 tca ctt gat aaa agc aaa ccc cac cta agc aaa gac ggc att aac gca 3120
 Ser Leu Asp Lys Ser Lys Pro His Leu Ser Lys Asp Gly Ile Asn Ala
 1025 1030 1035 1040

FIG.8L

ggt ggt aaa aag att acc aac att caa tca ggt gag att gcc caa aac 3168
 Gly Gly Lys Lys Ile Thr Asn Ile Gln Ser Gly Glu Ile Ala Gln Asn
 1045 1050 1055

agc cat gat gct gtg aca ggc ggc aag att tat gat tta aaa acc gaa 3216
 Ser His Asp Ala Val Thr Gly Gly Lys Ile Tyr Asp Leu Lys Thr Glu
 1060 1065 1070

ctt gaa aac aaa atc agc agt act gcc aaa aca gca caa aac tca tta 3264
 Leu Glu Asn Lys Ile Ser Ser Thr Ala Lys Thr Ala Gln Asn Ser Leu
 1075 1080 1085

cac gaa ttc tca gta gca gat gaa caa ggt aat aac ttt acg gtt agt 3312
 His Glu Phe Ser Val Ala Asp Glu Gln Gly Asn Asn Phe Thr Val Ser
 1090 1095 1100

aac cct tac tcc agt tat gac acc tca aag acc tct gat gtc atc acc 3360
 Asn Pro Tyr Ser Ser Tyr Asp Thr Ser Lys Thr Ser Asp Val Ile Thr
 1105 1110 1115 1120

ttt gca ggt gaa aac ggc att acc acc aag gta aat aaa ggt gtg gtg 3408
 Phe Ala Gly Glu Asn Gly Ile Thr Thr Lys Val Asn Lys Gly Val Val
 1125 1130 1135

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FIG. 8M

cgt gtg ggc att gac caa acc aaa ggc tta acc acg cct aag ctg acc 3456
 Arg Val Gly Ile Asp Gln Thr Lys Gly Leu Thr Thr Pro Lys Leu Thr
 1140 1145 1150

gtg ggt aat aat ggc aaa ggc att gtc att gac agc caa aat ggt 3504
 Val Gly Asn Asn Gly Lys Gly Ile Val Ile Asp Ser Gln Asn Gly
 1155 1160 1165

caa aat acc atc aca gga cta agc aac act cta gct aat gtt acc aat 3552
 Gln Asn Thr Ile Thr Gly Leu Ser Asn Thr Leu Ala Asn Val Thr Asn
 1170 1175 1180

gat aaa ggt agc gta cgc acc aca gaa cag ggc aat ata atc aaa gac 3600
 Asp Lys Gly Ser Val Arg Thr Thr Glu Gln Gly Asn Ile Ile Lys Asp
 1185 1190 1195 1200

gaa gac aaa acc cgt gcc gcc agc att gtt gat gtg cta agc gca ggc 3648
 Glu Asp Lys Thr Arg Ala Ala Ser Ile Val Asp Val Leu Ser Ala Gly
 1205 1210 1215

ttt aac ttg caa ggc aat ggt gaa ggc gtt gac ttt gtc toc act tat 3696
 Phe Asn Leu Gln Gly Asn Gly Glu Ala Val Asp Phe Val Ser Thr Tyr
 1220 1225 1230

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FIG.8N

gac acc gtc aac ttt gcc gat ggc aat gcc acc acc gct aag gtg acc 3744
 Asp Thr Val Asn Phe Ala Asp Gly Asn Ala Thr Thr Ala Lys Val Thr
 1235 1240 1245
 tat gat gac aca agc aaa acc agt aaa gtg gtc tat gat gtc aat gtg 3792
 Tyr Asp Asp Thr Ser Lys Thr Ser Lys Val Val Tyr Asp Val Asn Val
 1250 1255 1260
 gat gat aca acc att gaa gtt aaa gat aaa aaa ctt ggc gta aaa acc 3840
 Asp Asp Thr Thr Ile Glu Val Lys Lys Asp Lys Lys Leu Gly Val Lys Thr
 1265 1270 1275 1280
 acc aca ttg acc agt act ggc aca ggt gct aat aaa ttt gcc cta agc 3888
 Thr Thr Leu Thr Ser Thr Gly Thr Gly Ala Asn Lys Phe Ala Leu Ser
 1285 1290 1295
 aat caa gct act ggc gat gcg ctt gtc aag gcc agt gat atc gtt gct 3936
 Asn Gln Ala Thr Gly Asp Ala Leu Val Lys Ala Ser Asp Ile Val Ala
 1300 1305 1310
 cat cta aac acc tta tct ggc gac atc caa act gcc aaa ggg gca agc 3984
 His Leu Asn Thr Leu Ser Gly Asp Ile Gln Thr Ala Lys Gly Ala Ser
 1315 1320 1325

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FIG.80

caa gog aac aac tca gca ggc tat gtg gat gct gat ggc aat aag gtc 4032
 Gln Ala Asn Asn Ser Ala Gly Tyr Val Asp Ala Asp Gly Asn Lys Val
 1330 1335 1340

atc tat gac agt acc gat aac aag tac tat caa gcc aaa aat gat ggc 4080
 Ile Tyr Asp Ser Thr Asp Asn Lys Tyr Tyr Gln Ala Lys Asn Asp Gly
 1345 1350 1355 1360

aca gtt gat aaa acc aaa gaa gtt gcc aaa gac aaa ctg gtc gcc caa 4128
 Thr Val Asp Lys Thr Lys Glu Val Ala Lys Asp Lys Leu Val Ala Gln
 1365 1370 1375

gcc caa acc cca gat ggc aca ttg gct caa atg aat gtc aaa tca gtc 4176
 Ala Gln Thr Pro Asp Gly Thr Leu Ala Gln Met Asn Val Lys Ser Val
 1380 1385 1390

att aac aaa gaa caa gta aat gat gcc aat aaa aag caa ggc atc aat 4224
 Ile Asn Lys Glu Gln Val Asn Asp Ala Asn Lys Lys Gln Gly Ile Asn
 1395 1400 1405

gaa gac aac gcc ttt gtt aaa gga ctt gaa aaa gcc gct tct gat aac 4272
 Glu Asp Asn Ala Phe Val Lys Gly Leu Glu Lys Ala Ala Ser Asp Asn
 1410 1415 1420

FIG.8P

aaa acc aaa aac gcc gca gta act gtg ggt gat tta aat gcc gtt gcc 4320
 Lys Thr Lys Asn Ala Ala Val Thr Val Gly Asp Leu Asn Ala Val Ala 1440
 1425 1430 1435
 caa aca cag ctg acc ttt gca ggg gat aca ggc aca acg gct aaa aaa 4368
 Gln Thr Pro Leu Thr Phe Ala Gly Asp Thr Gly Thr Thr Ala Lys Lys 1455
 1445 1450
 ctg ggc gag act ttg acc atc aaa ggt ggg caa aca gac acc aat aag 4416
 Leu Gly Glu Thr Leu Thr Ile Lys Gly Gly Gln Thr Asp Thr Asn Lys 1470
 1460 1465
 cta acc gat aat aac atc ggt gtg gta gca ggt act gat ggc ttc act 4464
 Leu Thr Asp Asn Asn Ile Gly Val Val Ala Gly Thr Asp Gly Phe Thr 1485
 1475 1480
 gtc aaa ctt gcc aaa gac cta acc aat ctt aac agc gtt aat gca ggt 4512
 Val Lys Leu Ala Lys Asp Leu Thr Asn Leu Asn Ser Val Asn Ala Gly 1500
 1490 1495
 ggc acc aaa att gat gac aaa ggc gtg tct ttt gta gac tca agc ggt 4560
 Gly Thr Lys Ile Asp Asp Lys Gly Val Ser Phe Val Asp Ser Ser Gly 1520
 1505 1510 1515

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FIG.8Q

caa gcc aaa gca aac acc cct gtg cta agt gcc aat ggg ctg gac ctg 4608
 Gln Ala Lys Ala Asn Thr Pro Val Leu Ser Ala Asn Gly Leu Asp Leu 1535
 1525 1530

ggt ggc aag gtc atc agt aat gtg ggc aaa ggc aca aaa gat acc gac 4656
 Gly Gly Lys Val Ile Ser Asn Val Gly Lys Gly Thr Lys Asp Thr Asp 1550
 1540 1545

gct gcc aat gta caa cag tta aac gaa gta ggc aac ttg ttg ggt ctt 4704
 Ala Ala Asn Val Gln Gln Leu Asn Glu Val Arg Asn Leu Leu Gly Leu 1565
 1555 1560

ggt aat gct ggt aat gat aac gct gac ggc aat cag gta aac att gcc 4752
 Gly Asn Ala Gly Asn Asp Asn Ala Asp Gly Asn Gln Val Asn Ile Ala 1580
 1570 1575

gac atc aaa aaa gac cca aat tca ggt tca tct aac cgc act gtc 4800
 Asp Ile Lys Lys Asp Pro Asn Ser Gly Ser Ser Ser Asn Arg Thr Val 1600
 1585 1590 1595

atc aaa gca ggc acg gta ctt ggc ggt aaa ggt aat aac gat acc gaa 4848
 Ile Lys Ala Gly Thr Val Leu Gly Gly Lys Gly Asn Asn Asp Thr Glu 1615
 1605 1610

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FIG.8R

aaa ctt gcc act ggt ggt ata caa gtg ggc ggc gat aaa gac ggc aac 4896
 Lys Leu Ala Thr Gly Gly Ile Gln Val Gly Val Asp Lys Asp Gly Asn 1620 1625 1630

 gct aac ggc gat tta agc aat gtt tgg gtc aaa acc caa aaa gat ggc 4944
 Ala Asn Gly Asp Leu Ser Asn Val Trp Val Lys Thr Gln Lys Asp Gly 1635 1640 1645

 agc aaa aaa gcc ctg ctc gcc act tat aac gcc gca ggt cag acc aac 4992
 Ser Lys Lys Ala Leu Leu Ala Thr Tyr Asn Ala Ala Gly Gln Thr Asn 1650 1655 1660

 tat ttg acc aac aac ccc gca gaa gcc att gac aga ata aat gaa caa 5040
 Tyr Leu Thr Asn Asn Pro Ala Glu Ala Ile Asp Arg Ile Asn Glu Gln 1665 1670 1675 1680

 ggt atc cgc ttc ttc cat gtc aac gat ggc aat caa gag cct gtg gta 5088
 Gly Ile Arg Phe Phe His Val Asn Asp Gly Asn Gln Glu Pro Val Val 1685 1690 1695

 caa ggg cgt aac ggc att gac tca agt gcc tca ggc aag cac tca gtg 5136
 Gln Gly Arg Asn Gly Ile Asp Ser Ser Ala Ser Gly Lys His Ser Val 1700 1705 1710

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FIG.8S

ggc ata ggt ttc cag gcc aag gca gat ggt gaa gcc gcc gtt gcc ata 5184
 Ala Ile Gly Phe Gln Ala Lys Ala Asp Gly Glu Ala Ala Val Ala Ile
 1715 1720 1725

ggc aga caa acc caa gca ggc aac caa tcc atc gcc atc ggt gat aac 5232
 Gly Arg Gln Thr Gln Ala Gly Asn Gln Ser Ile Ala Ile Gly Asp Asn
 1730 1735 1740

gca caa gcc aag ggc gat caa tcc atc gcc atc ggt aca ggc aat gtg 5280
 Ala Gln Ala Thr Gly Asp Gln Ser Ile Ala Ile Gly Thr Gly Asn Val
 1745 1750 1755 1760

gta gca ggt aag cac tct ggt gcc atc ggc gac cca agc act gtt aag 5328
 Val Ala Gly Lys His Ser Gly Ala Ile Gly Asp Pro Ser Thr Val Lys
 1765 1770 1775

gct gat aac agt tac agt gtg ggt aat aac aac cag ttt acc gat gcc 5376
 Ala Asp Asn Ser Tyr Ser Val Gly Asn Asn Asn Gln Phe Thr Asp Ala
 1780 1785 1790

act caa acc gat gtc ttt ggt gtg ggc aat aac atc acc gtg acc gaa 5424
 Thr Gln Thr Asp Val Phe Gly Val Gly Asn Asn Ile Thr Val Thr Glu
 1795 1800 1805

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FIG.8T

agt aac tog gtt gcc tta ggt tca aac tct gcc atc agt gca ggc aca 5472
 Ser Asn Ser Val Ala Leu Gly Ser Asn Ser Ala Ile Ser Ala Gly Thr
 1810 1815 1820

cac gca ggc aca caa gcc aaa aaa tct gac ggc aca gca ggt aca acc 5520
 His Ala Gly Thr Gln Ala Lys Lys Ser Asp Gly Thr Ala Gly Thr Thr
 1825 1830 1835 1840

acc aca gca ggt gca acc ggt aog gtt aaa ggc ttt gct gga caa aog 5568
 Thr Thr Ala Gly Ala Thr Gly Thr Val Lys Gly Phe Ala Gly Gln Thr
 1845 1850 1855

gog gtt ggt gog gtc tcc gtg ggt gcc tca ggt gct gaa cgc cgt atc 5616
 Ala Val Gly Ala Val Ser Val Gly Ala Ser Gly Ala Glu Arg Arg Ile
 1860 1865 1870

caa aat gtg gca gca ggt gag gtc agt gcc acc agc acc gat gog gtc 5664
 Gln Asn Val Ala Ala Gly Glu Val Ser Ala Thr Ser Thr Asp Ala Val
 1875 1880 1885

aat ggt agc cag ttg tac aaa gcc acc caa agc att gcc aac gca acc 5712
 Asn Gly Ser Gln Leu Tyr Lys Ala Thr Gln Ser Ile Ala Asn Ala Thr
 1890 1895 1900

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FIG.8U

aat gag ctt gac cat cgt atc cac caa aac gaa aat aag gcc aat gca Asn Glu Leu Asp His Arg Ile His Gln Asn Glu Asn Lys Ala Asn Ala 1905 1910 1915 1920	5760
ggg att tca tca gcg atg gcg atg gcg tcc atg cca caa gcc tac att Gly Ile Ser Ser Ala Met Ala Met Ala Ser Met Pro Gln Ala Tyr Ile 1925 1930 1935	5808
cct ggc aga tcc atg gtt acc ggg ggt att gcc acc cac aac ggt caa Pro Gly Arg Ser Met Val Thr Gly Gly Ile Ala Thr His Asn Gly Gln 1940 1945 1950	5856
ggt gcg gtg gca gtg gga ctg tog aag ctg tog gat aat ggt caa tgg Gly Ala Val Ala Val Gly Leu Ser Lys Leu Ser Asp Asn Gly Gln Trp 1955 1960 1965	5904
gta ttt aaa atc aat ggt tca gcc gat acc caa ggc cat gta ggg gcg Val Phe Lys Ile Asn Gly Ser Ala Asp Thr Gln Gly His Val Gly Ala 1970 1975 1980	5952
gca gtt ggt gca ggt ttt cac ttt taagccataa atogcaagat ttactttaa Ala Val Gly Ala Gly Phe His Phe 1985 1990	6006

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FIG.8V

aatcaatctc accatagttg tataaaacag catcagcatc agtcatatta ctgatgctga 6066
tgttttttat cacttaaacc attttacgc tcaagtgatt ctctttcacc atgaccacaaat 6126
cgccattgat cataggtaaa cttattgagt aaattttatc aatgtagttg ttagatatgg 6186
ttaaaattgt gccattgacc aaaaaatgac cgatttatcc ogaaaaatttc tgattatgat 6246
cogttgacct gca 6259

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Construction of pKS294

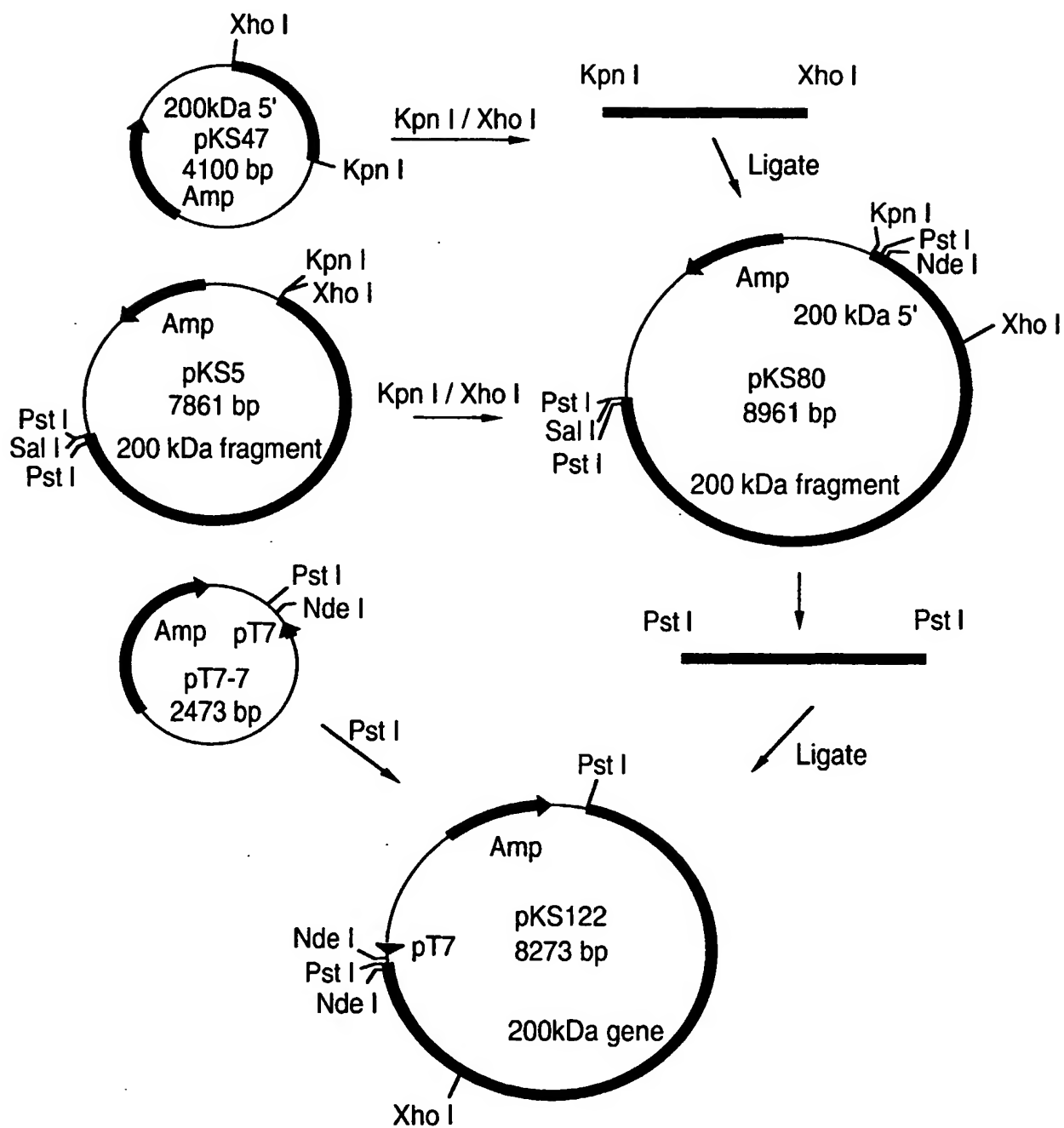


FIG.9A

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Construction of pKS294

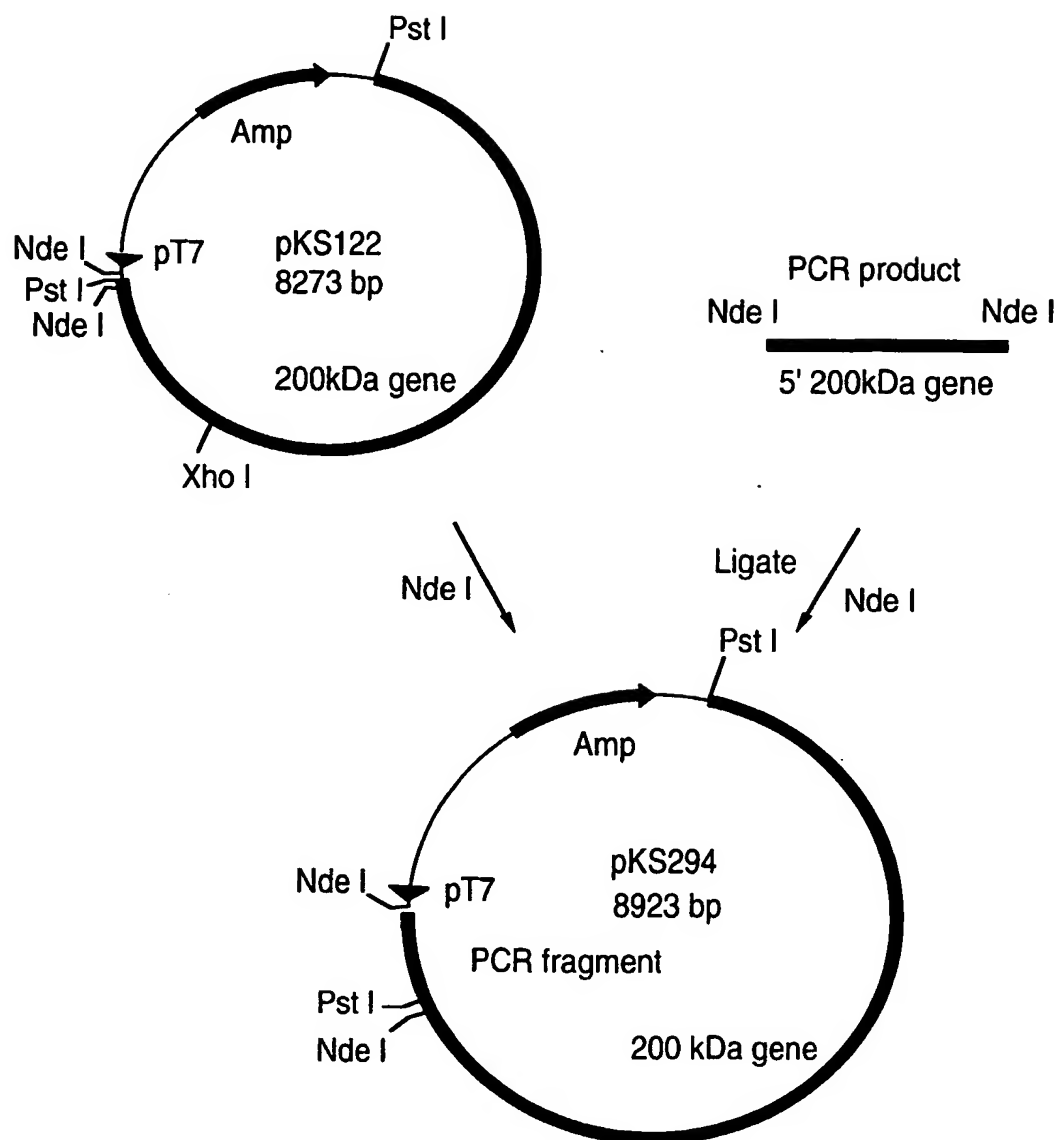


FIG.9B

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Construction of pKS348

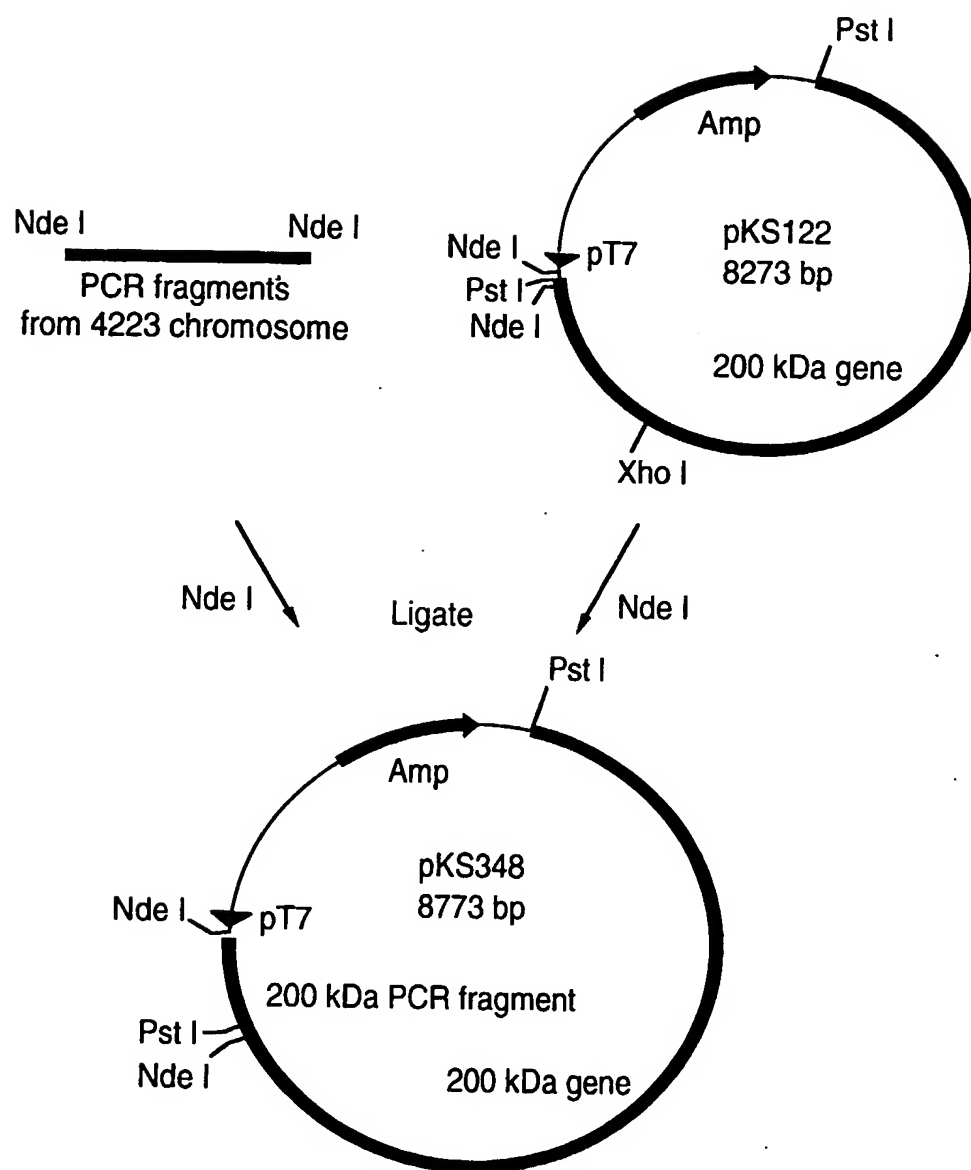


FIG.10

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Purification of r200 kDa Protein from E. coli

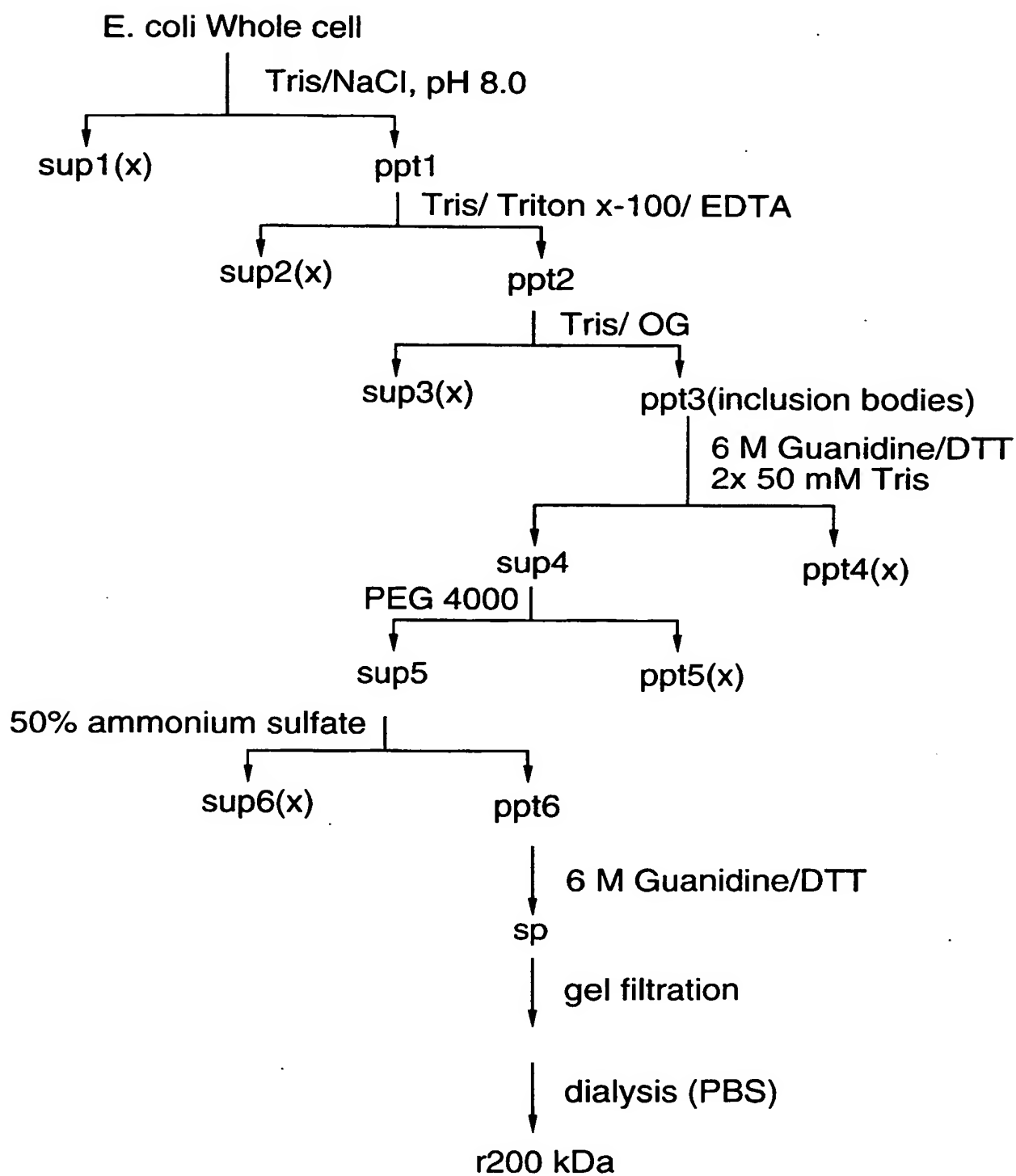
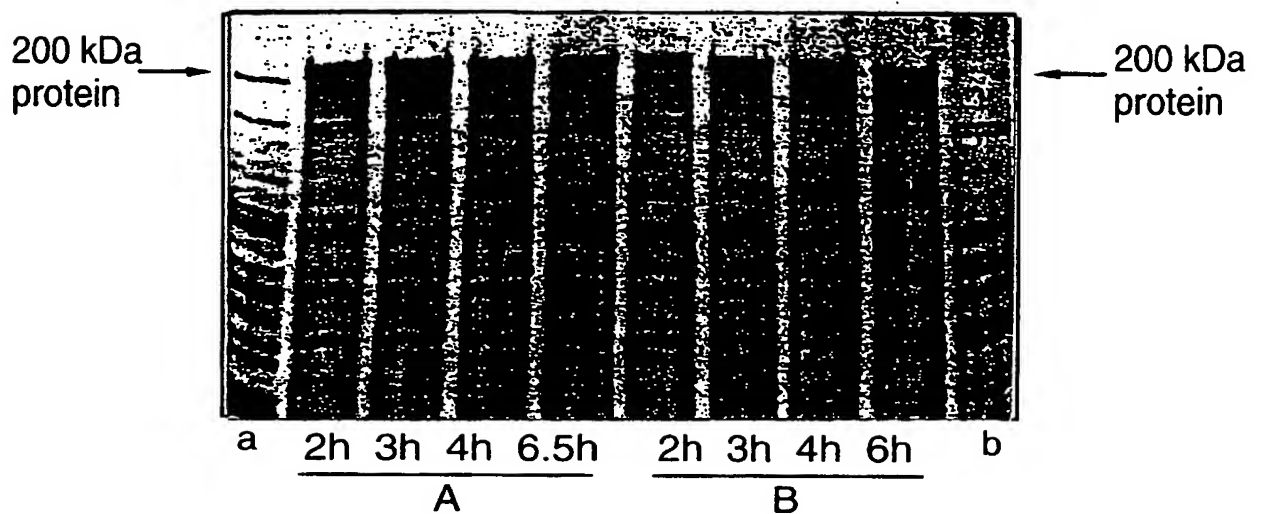


FIG.11

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Expression of M 56 r200 kDa Protein Gene in E. coli



A: KS358 induced when O.D. at 600nm was 0.26

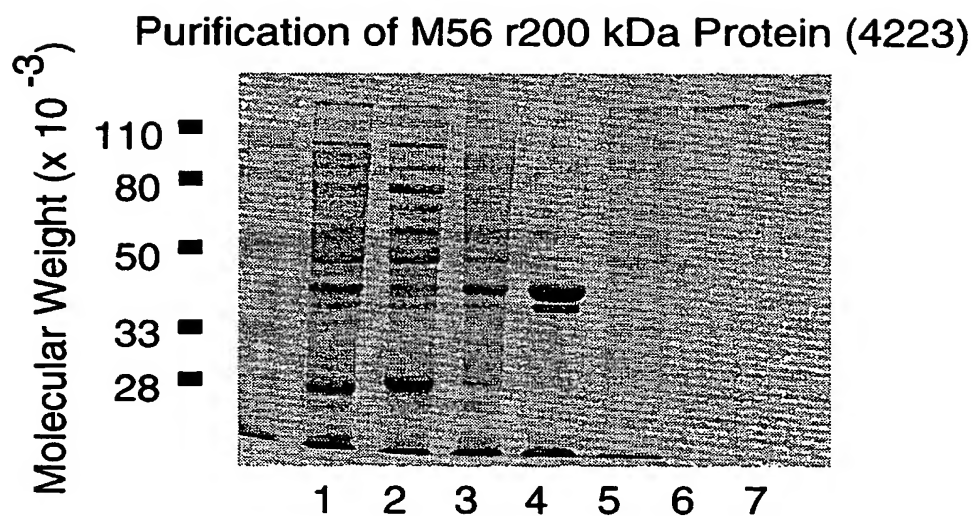
B: KS358 induced when O.D. at 600nm was 0.44

a: strain 4223 lysate

b: KS358 cultured overnight

FIG.12

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1. E. coli Whole cells
2. Soluble proteins after 50mM Tris/ NaCl, pH 8, extraction
3. Soluble proteins after Tris/ Triton X-100/ EDTA extraction
4. Soluble proteins after Tris/ OG extraction
5. Pellet after Tris/ OG extraction
- 6-7. Purified 200 kDa protein

FIG.13

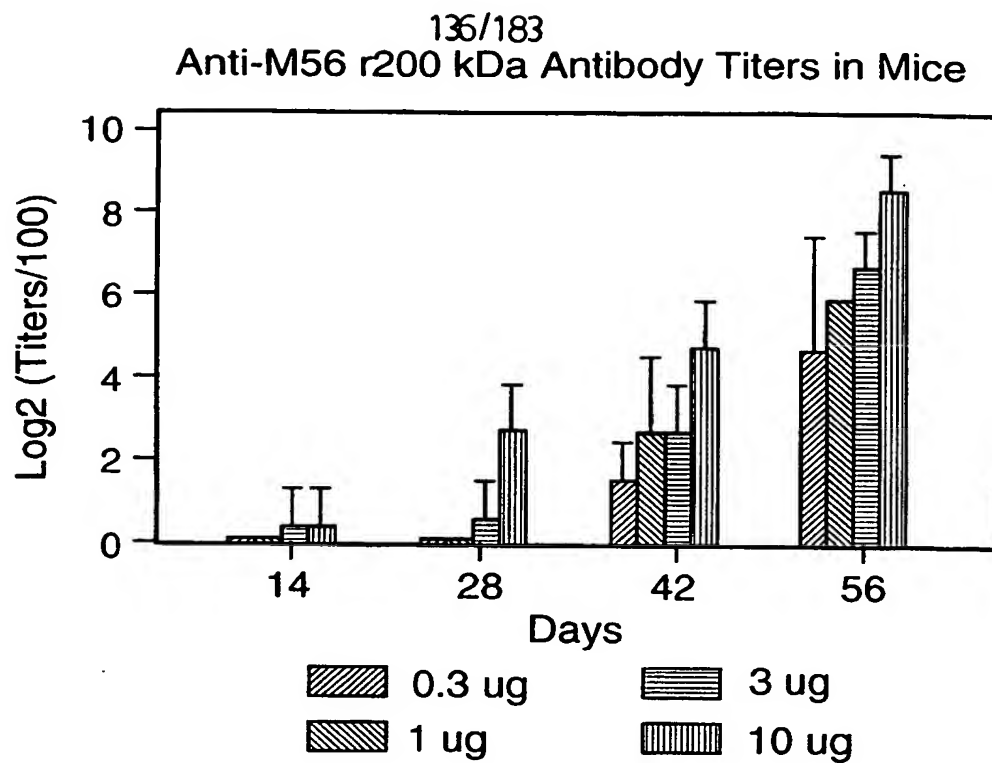


FIG.14

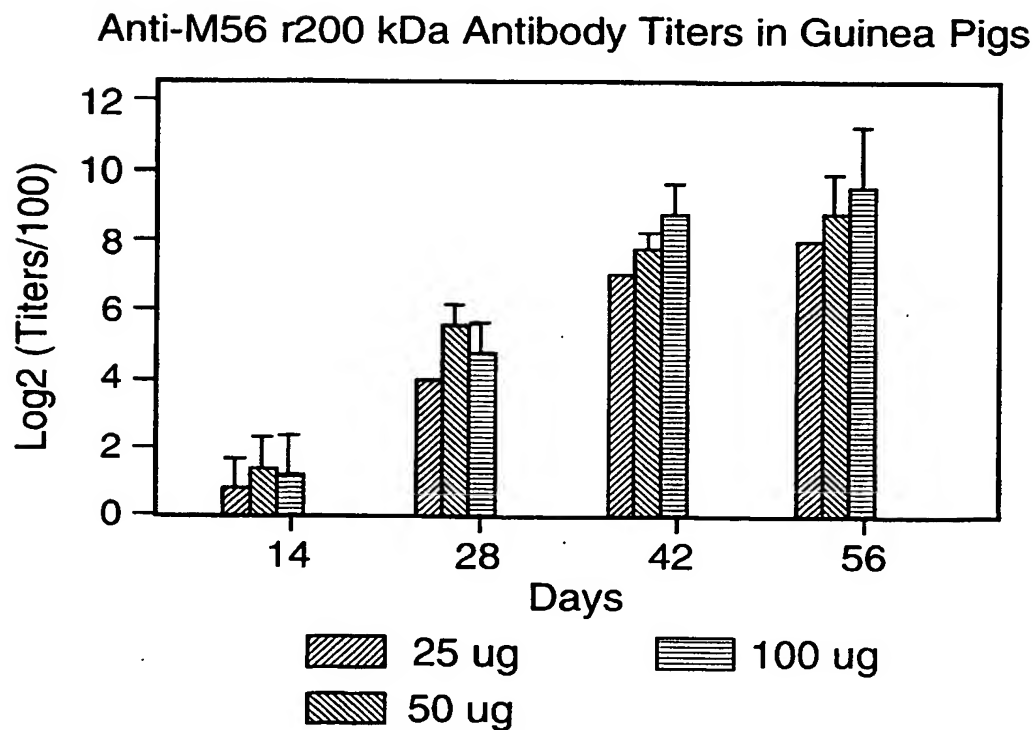


FIG.15

PCR amplification of DNA fragments carrying a portion of the 200 kDa protein gene from chromosomal DNA of RH408

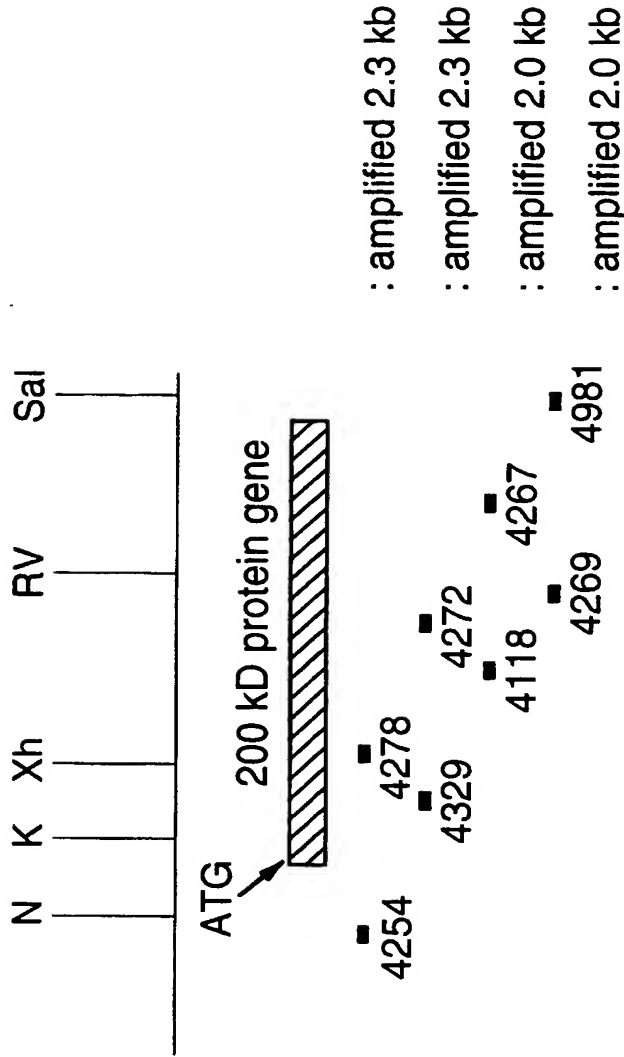


FIG.16

FIG.17A

M. catarrhalis strain 4223 200 kDa

```
CCATGGATATGGGCAAGTGTCCTCGCCCTGC      10      30
... CGTATGATGGCGGATGACACCCCATTTGCCCC      40      60
...                                     50

CATATCTGTACGATTTGACATGTGATATGA      70      90
... TTTAACATGTGACATGATTTAACATTTGTTT      100     120
...                                     110     138/183

AATACGTGTGCCATCATTAACCAATAATTAG      130     150
... TAACGCATTTAGTAACGCATTTGTAAAAAT      160     180
...                                     170

CATTGCGCCCTTTATGTGTATCATATGAA      190     210
```

FIG.17B

... TAGAATAATGATTTGTA TCTGATTTATTTGT 240
 ... 220 230

ATCAGAAATGGTGCTATATGATGATGCC 260
 ... TACGAGTTGATTTGGGTTAATCACTCTATG 300
 ... 280 290

ATTGATAATTTTGAAACATAATCTATTGA 310
 ... CTTAAATCACCATATGGTTAATAATTAGCA 360
 ... 320 330 340 350

TAA TGGTAGGCTTTTGTAAATAACACATC 370
 ... GCAATAATTGTTCTACTGT TACCTACCATGCT 420
 ... 380 390 400 410

TGAATGACGATCCCCAATCACCATTCATT 430
 ... 440 450

FIG.17C

... CAAGTGATGTGTTTGTATACGCACCATTTA 480
 ... 460

CCCTAATTATTCAATCAAAATGCCCTATGTC 490
 ... 510
 ... AGCATGTATCATTTTTTTAAGGTAAACCAC 540
 ... 520

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MET ASN HIS ILE TYR LYS VAL ILE PHE ASN
 CATGAATCACATCTATAAAGTCATCTTTAA 550
 ... 560
 ... LYS ALA¹² THR GLY THR PHE MET ALA VAL¹⁹ ALA
 ...CAAAGCCACAGGCACATTTATGGCAGTGGC 600
 ... 580

GLU TYR ALA LYS SER HIS SER THR GLY GLY
 AGAGTACGCCAAATCCACAGCACGGGGG 630
 ... 610

FIG.17D

... GLY SER CYS ALA THR GLY GIN VAL GLY³⁹ SER
 ...GGGTAGCTGTGCTACAGGGCAAGTTGGCAG 660
 ... 640
 VAL CYS THR LEU SER PHE ALA ARG ILE ALA
 TGTATGCACTCTGAGCCTTTGCCCGTATTGC 680
 ... 670
 ... ALA LEU ALA VAL LEU VAL⁵⁶ ILE GLY ALA THR
 ...CGCGCTCGCTGTCTCGTGATCGGTGCAAC 720
 ... 700
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3' Half Constructs Of 200 kD Protein Gene

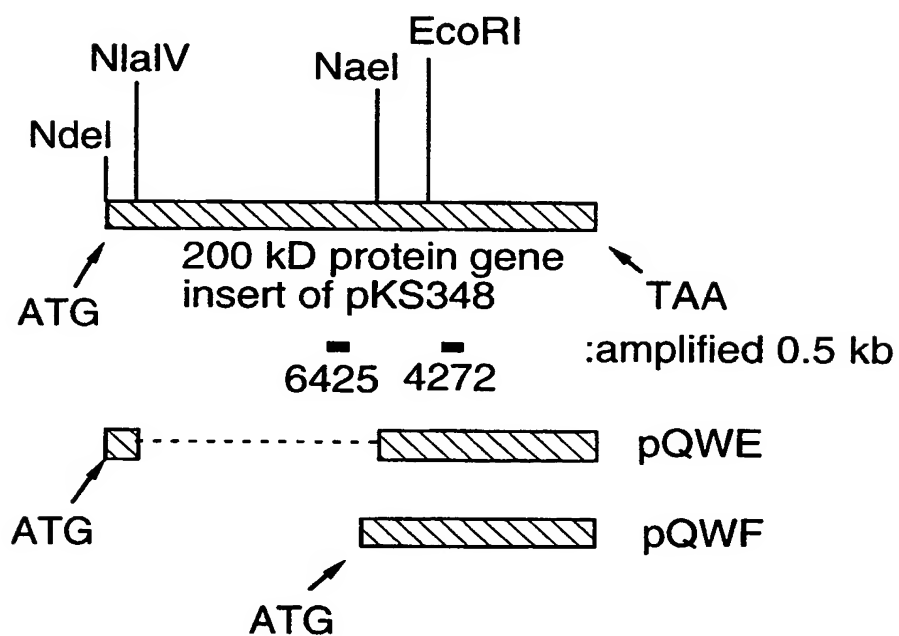


FIG.18

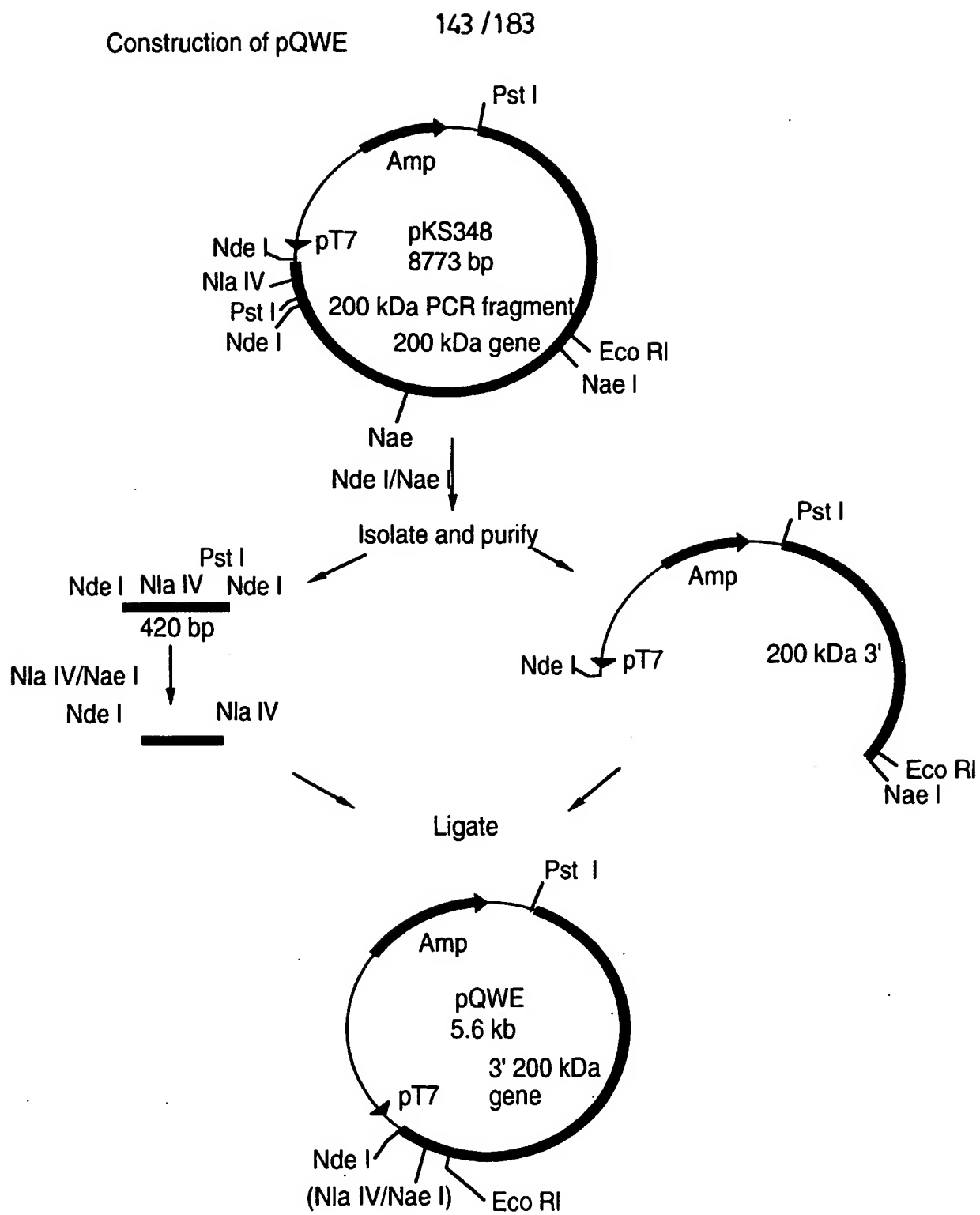


FIG.19

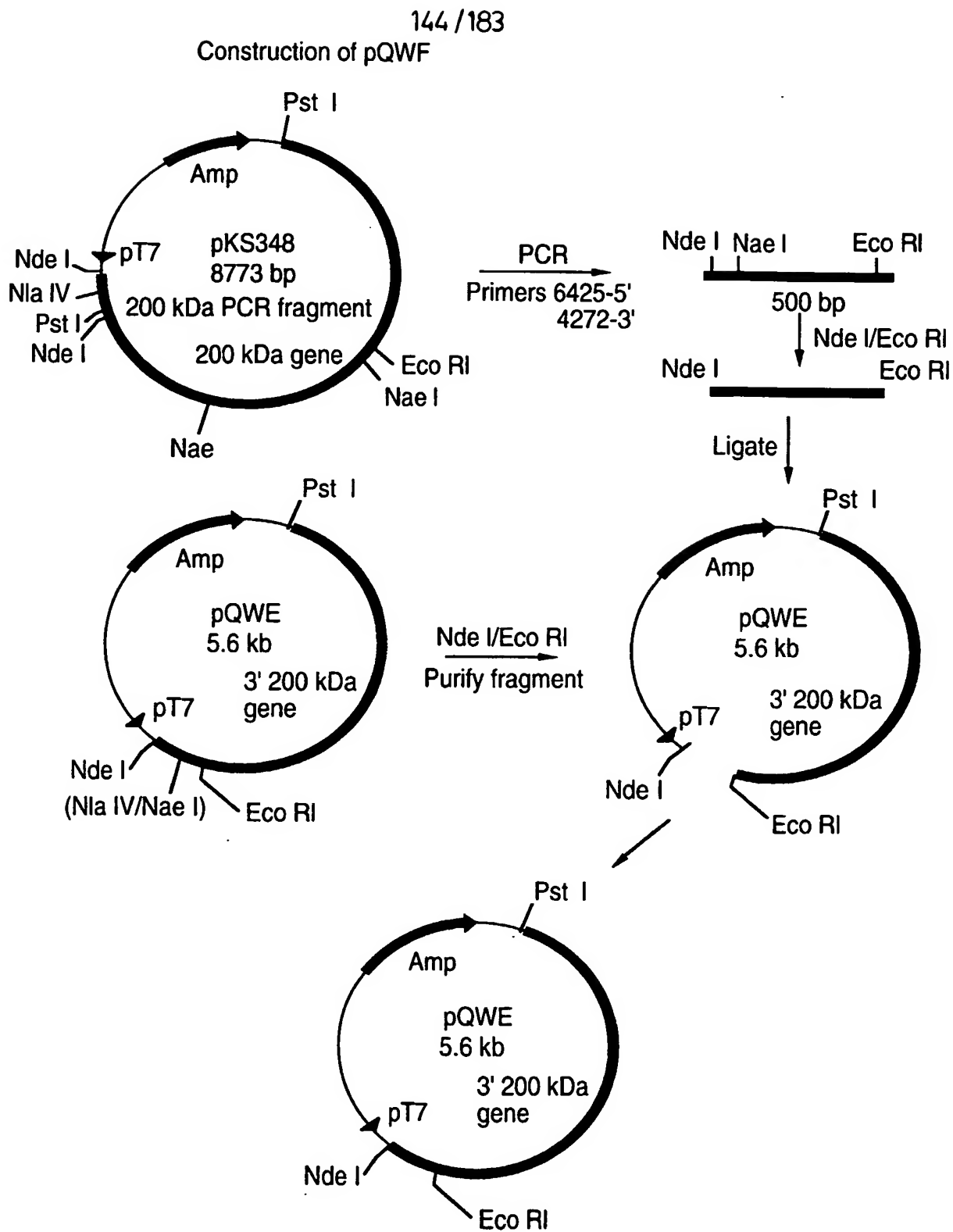


FIG.20

FIG.21A

M. catarrhalis strain 4223 200 kDa gene

```

CCA TGG ATA TGG GCA GGT GTG C TCG CCT GC ...
10          20          30 ...
...CGT ATG ATG GCG ATG ACA CCCC ATTTG CCCC
40          50          60

CAT ATC TGT AC GAT TTG ACA TGT GAT ATGA ...
70          80          90 ...
...TTA ACA TGT GACA TGA TTAA CA TTGT TT
100         110        120

AAT ACT GTT GCC CAT CAT TAC CAT AAT TTAG ...
130        140        150 ...
...TAA CGCA TTTAG TAA CGCA TTGT AAAAAT
160        170        180

CAT TGC GCG CCC CTTTAT GTGT ATCAT ATGAA ...
190        200        210 ...

```

FIG.21B

```

...TAGAATAATTATGATTGTTATCTGATTATTGT      240
...      220

ATCAGAAATGGTGATGCTATATGATGATGCC ...
250      260      270 ...
...TACGAGTTGATTGGGTTAATCACTCTATG      300
...      280      290

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ATTGATAATAATTTGAAACATAATCTATTGA ...
310      320      330 ...
...CTTAAATCACCATATGGTTATAATTTAGCA      360
...      340      350

TAATGGTAGGCTTTTGTAAATAATCACATC ...
370      380      390 ...
...GCAATAATTGTTCTACTGTACTACCATGCT      420
...      400      410

```

FIG.21C

```

TGAATGACGATCCCAATCACCAGATTCA TT ... 440
430                                     450 ...
...CAAGTGATGTGTTTGTATACGCCACCA TT TA 460
...                                     470
                                     480

CCCTAATTA TTTCAAATCAAAATGCCCTATGTC ... 490
500                                     510 ...
...AGCATGTATCATTTT TTAAGGTA AACCA C 520
...                                     530
                                     540 147/183

MET ASN HIS ILE TYR LYS VAL ILE PHE ASN...
CATGAATCACA TCTATAAAGTCA TCTTTAA ... 550
560                                     570 ...
... LYS ALA THR GLY THR PHE MET ALA VAL ALA
...CAAAGCCACAGGCCACATTTATGGCAGTGGC 580
...                                     590
                                     600

GLU TYR ALA LYS SER HIS SER THR GLY GLY...
AGAGTACGCCCAAATCCCAACAGCACGGGGG ... 610
620                                     630 ...
... GLY SER CYS ALA THR GLY GLN VAL GLY SER
...GGGTAGCTGTGCTACAGGCCAAGTTGGCAG 640
...                                     650
                                     660

```

FIG. 21D

VAL CYS THR LEU SER PHE ALA ARG ILE ALA...
TGTATGCACCTCTGAGCTTTGCCCGTATTGC...
670 680 690 ...

pKS348 →
...
... ALA LEU ALA VAL LEU VAL ILE GLY ALA THR
...CGCGCTCGCTGTCCTCGTGATCGGTGCAAC
... 700 710 720

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LEU SER GLY SER ALA TYR ALA GLN LYS LYS...
GCTCAGTGGCAGTGCTTATTGCTCAAAATAA...
730 740 750 ...

... ASP THR LYS HIS ILE ALA ILE GLY GLU GLN
...AGATAACCAACAATATCGCAATTGGTGACA
... 760 770 780

ASN GLN PRO ARG ARG SER GLY THR ALA LYS...
AACCAGCCAGACGCTCAGGCACTGCCAA...
800 810 ...

... ALA ASP GLY ASP ARG ALA ILE ALA ILE GLY
...GGCGGACGGTGATCGAGCCATTGCTATTGG
... 820 840

FIG.21E

```

      GLU ASN ALA ASN ALA GIN GLY GLY GIN ALA...
      TGAAAATGCTAACGCACAGGCGGTCAAGC...
      850                                     860 ...
            ... ILE ALA ILE GLY SER SER ASN LYS THR VAL
            ...CATCGCCATC GGTAGTAGTAATAAAACTGT
            ...                                     880
            ...                                     890
      ASN GLY SER SER LEU ASP LYS ILE GLY THR...
      CAATGGAGCAGTTTGGAATAAGATAGGTAC...
      910                                     920 ...
            ... ASP ALA THR GLY GIN GLU SER ILE ALA ILE
            ...CGATGCTACGGGTCAAGAGTCCATCGCCAT
            ...                                     940
            ...                                     950
            ...                                     960
      GLY GLY ASP VAL LYS ALA SER GLY ASP ALA...
      CGGTGGTGATGTAAAGGCTAGTGGTGATGC...
      970                                     980 ...
            ... SER ILE ALA ILE GLY SER SER ASP ASP LEU HIS
            ...CTCGATTGCCATCGGGTAGTGATGACTTACA
            ...                                     1000
            ...                                     1010
            ...                                     1020

```

FIG.21F

```

LEU LEU ASP GLN HIS GLY ASN PRO LYS HIS...
TTTGCTTGATCAGCATGGTAATCCCTAAACA ...
1030                               1040
... PRO LYS GLY THR LEU ILE ASN ASP LEU ILE
...TCCGAAGGTACTCTGATTTAACGATCTTAT
1060                               1070
...                               1080

ASN GLY HIS ALA VAL LEU LYS GLU ILE ARG...
TAACGGCCATGCAGTATTAAAGAAATACG ...
1090                               1100
... SER SER LYS ASP ASN ASP VAL LYS TYR ARG
...AAGCTCAAGGATAATGATGTAATAATAG
1120                               1130
...                               1140

ARG THR THR ALA SER GLY HIS ALA SER THR...
ACGCACAACCGCAAGCGGACACGCCAGTAC ...
1150                               1160
... ALA VAL GLY ALA MET SER TYR ALA GLN GLY
...TGCA GTGGAGCCATGTCATATGCACAGGG
1180                               1190
...                               1200

HIS PHE SER ASN ALA PHE GLY THR ARG ALA...
TCATTTTCCCAACGCCCTTTGGTACACGGGC ...
1210                               1220
...                               1230

```

FIG.21G

... THR ALA LYS SER ALA TYR SER LEU ALA VAL
 ...A A C A G C C T A A A A G T G C C C T A T T C C C T T G G C A G T
 ... 1240 1250 1260

GLY LEU ALA ALA THR ALA GLU GLY GLN SER...
 G G G T C T T G C C G C C A C A G C C G A G G C C A A T C ...
 1270 1280 1290 ...

... THR ILE ALA ILE GLY SER ASP ALA THR SER
 ...T A C A A T C G C T A T T G G T T C T G A T G C A A C A T C
 ... 1300 1310 1320 151/183

SER SER LEU GLY ALA ILE ALA LEU GLY ALA...
 T A G C T C G T T G G G A G C G A T A G C C C T T G G T G C ...
 1330 1340 1350 ...

... GLY THR ARG ALA GLN LEU GLN GLY SER ILE
 ...A G G T A C T C G T G C T C A G C T A C A G G G C A G T A T
 ... 1360 1370 1380

ALA LEU GLY GLN GLY SER VAL THR GLN...
 T G C C C T A G G T C A A G G T T C T G T T G T C A C T C A ...
 1390 1400 1410 ...

... SER ASP ASN ASN SER ARG PRO ALA TYR THR
 ...G A G T G A T A A T A A T T C T A G A C C G G C C T A T A C
 ... 1420 1430 1440

FIG.21H

```

PRO ASN THR GLN ALA LEU ASP PRO LYS PHE...
ACC A A T A C C C A G G C A C T A G A C C C C A A G T T ...
1450                                     1460 1470 ...
... GLN ALA THR ASN ASN THR LYS ALA GLY PRO
...T C A A G C C A C C A A T A A T A C G A A G G C G G T C C
1480                                     1490 1500
...
LEU SER ILE GLY SER ASN SER ILE LYS ARG...
ACT T T C C A T T G G T A G T A A C T C T A T C A A A C G ...
1510                                     1520 1530 ...
... LYS ILE ILE ASN VAL GLY ALA GLY VAL ASN
...T A A A T C A T C A A T G T C G G T G C A G G T G T T A A
1540                                     1550 1560
...
LYS THR ASP ALA VAL ASN VAL ALA GIN LEU...
T A A A C C G A T G C G G T C A A T G T G G C A C A G C T ...
1570                                     1580 1590 ...
... GLU ALA VAL VAL LYS TRP ALA LYS GLU ARG
...A G A A G C G G T G G T G A A G T G G G C T A A G G A G C G
1600                                     1610 1620
...
ARG ILE THR PHE GLN GLY ASP ASP ASN SER...
T A G A A T T A C T T T C A G G G T G A T G A T A A C A G ...
1630                                     1640 1650 ...

```

FIG.21I

```

...   THR ASP VAL LYS ILE GLY LEU ASP ASN THR
...TACTGACGTAAATAAGGTTTGGATAATAC      1680
...                                     1660
...
LEU THR ILE LYS GLY GLY ALA GLU THR ASN...
TTTAACTATTAAAGGTGGTGAGACCA A ...
1690                                     1700
...                                     1710 ...
...                                     possible truncation site 1
...   ALA LEU THR ASP ASN ILE GLY VAL VAL 153 / 183
...CGCATTAACCGATAATAATATCGGTGTGGT      1740
...                                     1720
...
LYS GLU ALA ASP ASN SER GLY LEU LYS VAL...
AAGAGGCTGATAATAAGTGGTCTGAAAGT ...
1750                                     1760
...   LYS LEU ALA LYS THR LEU ASN ASN LEU THR
...TAAACTTGCTAAACCTTTAAACAATCTTAC      1800
...                                     1780
...
GLU VAL ASN THR THR THR LEU ASN ALA THR...
TGAGGTGAATAACACTACATTAAATGCCAC ...
1810                                     1820
...                                     1830 ...

```

FIG.21J

```

...   THR   THR   VAL   LYS   VAL   GLY   SER   SER   SER   SER
...AACCAAGTTAAGGTAGGTAGTAGTAG
...
1840
1860

      THR   THR   VAL   LYS   VAL   GLY   SER   LEU...
TAC TAC AGC TGA ATTA TTGAGTGATAGTTT ...
1880
1890 ...

...   THR   PHE   THR   GLN   PRO   ASN   THR   GLY   SER   GLN
...AACCTTTACCCAGCCCAATACAGGCAGTCA
1900
1910
1920
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SER   THR   SER   LYS   THR   VAL   GLY   VAL   ASN...
AAGCACAAGCAAAACCGTCTATGGCGTTAA ...
1930
1940
1950 ...

...   GLY   VAL   LYS   PHE   THR   ASN   ASN   ALA   GLU   THR
...TGGGGTGAAAGTTTACTAATAATGCAGAAC
1960
1970
1980

      THR   ALA   ALA   ILE   GLY   THR   ARG   ILE   THR...
AACAGCAGCAATCGGCAC TACTCGTATTAC ...
1990
2000
2010 ...

...   ARG   ASP   LYS   ILE   GLY   PHE   ALA   ARG   ASP   GLY
...CAGAGATAAAATTGGCTTTGCTCGAGATGG
2020
2030
2040

```

FIG.21K

```

ASP VAL ASP GLU LYS GLN ALA PRO TYR LEU...
TGA TGT TGA TGA A A A C A A G C A C C A T A T T T ...
2050                               2060
... ASP LYS LYS GLN LEU LYS VAL GLY SER VAL
...GGATATAA A A A C A A C T T A A A G T G G G T A G T G T
...                               2080                2090                2100

ALA ILE THR ILE ASP ASN GLY ILE ASP ALA...
TGC AAT TACC ATAGAC AATGGCA TTGATGC ...
2110                               2120                2130 ...
... GLY ASN LYS LYS ILE SER ASN LEU ALA LYS
...AGGTATAATAAAGATCAGTAACTTGCCAA
...                               2140                2150                2160
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GLY SER SER ALA ASN ASP ALA VAL THR ILE...
AGGTAGCAGTGCTAACGATGCGGT TACCAT ...
2170                               2180                2190 ...
... GLU GLN LEU LYS ALA ALA LYS PRO THR LEU
...CGAACAGCTCAAGCCGCCAAGCCTACTTT
...                               2200                2210                2220

ASN ALA GLY ALA GLY ILE SER VAL THR PRO...
AACGCAGGCGCTGGCATCAGTGTCACACC ...
2230                               2240                2250 ...

```

FIG.21L

```

...   THR  GLU  ILE  SER  VAL  ASP  ALA  LYS  SER  GLY
...TACTGAATAATCAGTTGATGCTAAGAGTGG
...   2260   2270   2280

ASN  VAL  THR  ALA  PRO  THR  TYR  ASN  ILE  GLY...
CAATGTTACCGCCCCCACTTACAACATTGG ...
2290   2300   2310 ...
...   VAL  LYS  THR  THR  GLU  LEU  ASN  SER  ASP  GLY
...CGTGAAACCAACCGAGCTTAACAGTGATGG
...   2320   2330   2340   156/183

THR  SER  ASP  LYS  PHE  SER  VAL  LYS  GLY  SER...
CACTAGTGATAAATTAGTGTTAAGGTTAG ...
2350   2360   2370 ...
...   GLY  THR  ASN  ASN  SER  LEU  VAL  THR  ALA  GLU
...TGGTACGAACAATAAGCTTAGTTACCGCCGA
...   2380   2390   2400

HIS  LEU  ALA  SER  TYR  LEU  ASN  GLU  VAL  ASN...
ACATTTGGCAAGCTATCTAATAAGAGTCAA ...
2410   2420   2430 ...
...   ARG  THR  ALA  ASP  SER  ALA  LEU  GLN  SER  PHE
...TCGAACGGCTGACAGTGCTCTACAAGCTT
...   2440   2450   2460

```


FIG.21M

```

      THR  VAL  LYS  GLU  GLU  ASP  ASP  ASP  ASP  ALA...
      TACC GTTAAAGAGAGACGATGATGACGC ...
      2470      2480      2490 ...
      ...    ASN  ALA  ILE  THR  VAL  ALA  LYS  ASP  THR  THR
      ...CAACGCTATCACCGTGCGCTAAAGATACGAC
      ...      2500      2510      2520
      157/183
      LYS  ASN  ALA  GLY  ALA  VAL  SER  ILE  LEU  LYS...
      AAAAATGCCGCGCAGTCAGCATCTTAA ...
      2530      2540      2550 ...
      ...    LEU  LYS  GLY  LYS  ASN  GLY  LEU  THR  VAL  ALA
      ...ACTCAAGGTAAATAACGGTCTACGGTTGCTGC
      ...      2560      2570      2580
      THR  LYS  LYS  ASP  GLY  THR  THR  PHE  GLY...
      TACCAAAAGATGGTACGGTTACCTTTGG ...
      2590      2600      2610 ...
      ...    LEU  SER  GLN  ASP  SER  GLY  LEU  THR  ILE  GLY
      ...GCTTAGCCCAAGATAGCGGTCGTGACCATTTGG
      ...      2620      2630      2640
      LYS  SER  THR  LEU  ASN  ASN  ASP  GLY  LEU  THR...
      CAAAGCACCCCTAAACAACGATGGCTTGAC ...
      2650      2660      2670 ...

```

FIG.21N

```

... VAL LYS ASP THR ASN GLU GLN ILE GLN VAL
...TGT TAAAGATACCAACGAACAATCCAAGT
... 2680 2690 2700

GLY ALA ASN GLY ILE LYS PHE THR ASN VAL...
CGGTGCTAATGGCATTAAATTACTAATGT ...
2710 2720 2730 ...

... ASN GLY SER ASN PRO GLY THR GLY ILE ALA
...GAATGGTAGTAATCCAGGTACTGGCATTGC
... 2740 2750 2760 158/183

ASN THR ALA ARG ILE THR ARG ASP LYS ILE...
AATACCGCTCGCATTACCAGAGATAAAT ...
2770 2780 2790 ...

... GLY PHE ALA GLY SER ASP GLY ALA VAL ASP
...TGGCTTTGCTGGTTCTGATGGTGCA GTTGA
... 2800 2810 2820

THR ASN LYS PRO TYR LEU ASP GLN ASP LYS...
TACAACAACCTTATTCTTGATCAAGACA ...
2830 2840 2850 ...

... LEU GLN VAL GLY ASN VAL LYS ILE THR ASN
...GCTACAAGTTGGCAATGTTAAGATTACCAA
... 2860 2870 2880

```

FIG.210

```

THR  GLY  ILE  ASN  ALA  GLY  GLY  LYS  ALA  ILE...
CACTGGCATTACGCAGGTGGTAAAGCCAT...
2890                               2900
...      THR  GLY  LEU  SER  PRO  THR  LEU  PRO  SER  ILE
...CACAGGGCTGTCCCCAACACCTGCCCTAGCAT
...                               2920
2930
ALA  ASP  GLN  SER  SER  ARG  ASN  ILE  GLU  LEU...
TGCCGATCAAGTAGCCGCAACATAGAACT...
2950                               2960
...      GLY  ASN  THR  ILE  GLN  ASP  LYS  ASP  LYS  SER
...GGGCAATAACAATCCAGACAAAGACAAATC
...                               2980
ASN  ALA  ALA  SER  ILE  ASN  ASP  ILE  LEU  ASN...
CAACGCTGCCCAGCATTAAATGATATATAA...
3010                               3020
...      THR  GLY  PHE  ASN  LEU  LYS  ASN  ASN  ASN  ASN
...TACAGGCTTTAACCTAAATAATAACA
...                               3040
PRO  ILE  ASP  PHE  VAL  SER  THR  TYR  ASP  ILE...
CCCCATTGACCTTTGTCTCCACTTATGACAT...
3070                               3080

```

FIG.21P

... VAL ASP PHE ALA ASN GLY ASN ALA THR THR
 ...TGTGTGACTTTGCCCAATGGCAATGCCACCAC
 ... 3100 3110 3120

ALA THR VAL THR HIS ASP THR ALA ASN LYS...
 CGCCACAGTAACCCATGATACCGCTAACAA...
 3130 3140 3150 ...

... THR SER LYS VAL VAL TYR ASP VAL ASN VAL
 ...AACCAAGTAAGAAGTGGTATATGATGTGAATGT
 ... 3160 3170 3180

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ASP ASP THR THR ILE HIS LEU THR GLY THR...
 GGATGATACACCACTTCATCTAACAGGCAC...
 3190 3200 3210 ...

... ASP ASP ASN LYS LYS LEU GLY VAL LYS THR
 ...TGATGACAAATAAATACTTGGCGTCAAAAC
 ... 3220 3230 3240

THR LYS LEU ASN LYS THR SER ALA ASN GLY...
 CACCAACTGAAACAACAAGTGCTAATGG...
 3250 3260 3270 ...

... ASN THR ALA THR ASN PHE ASN VAL ASN SER
 ...TAATACAGCACTAACCTTAAATGTTAACTC
 ... 3280 3290 3300

FIG.21Q

```

SER  ASP  GLU  ASP  ALA  LEU  VAL  ASN  ALA  LYS...
TAGTGA  TGAAGA  TAGCCCTTGT  TACGCCAA  ...
3310                                     3320
...  ASP  ILE  ALA  GLU  ASN  LEU  THR  LEU  ALA
...AGACA  TCGCCGAA  AATCTAA  AACCCCTAGC
...                                     3340
                                     3350
                                     3360

LYS  GLU  ILE  HIS  THR  THR  LYS  GLY  THR  ALA...
CAGGAA  ATTCA  CACCA  CCAAGG  CACAGC  ...
3370                                     3380
...  ASP  THR  ALA  LEU  GLN  THR  PHE  THR  VAL  LYS
...AGACA  CCGCCCTACA  AACCTTTACCGTTAA
...                                     3400
                                     3410
                                     3420

LYS  VAL  ASP  GLU  ASN  ASN  ASN  ALA  ASP  ASP...
AAGGTAG  ATGA  AATA  ATAT  ATGCTGATGA  ...
3430                                     3440
...  ALA  ASN  ALA  ILE  THR  VAL  GLY  GLN  LYS  ASN
...CGCCA  ACGCCATCA  CCGTGGGTCAAAGA  A
...                                     3460
                                     3470
                                     3480

```

FIG.21R

ALA ASN ASN GLN VAL ASN THR LEU THR LEU...
 CGCAATAATCAAGTCAACCCCTAACACT...
 3490 3500 3510 ...
 ... LYS GLY GLU ASN GLY LEU ASN ILE LYS THR
 ...CAAAGGTGAACAACGGTCTTAATATTAAAC
 ... 3520 3530 3540

PQMF →

ASP LYS ASN GLY THR VAL THR PHE GLY ILE...
 CGACAAATAATGGTACGGTTACCTTTGGCAT...
 3550 3560 3570 ...
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... ASN THR THR SER GLY LEU LYS ALA GLY LYS
 ...TAACACCAACAAGCGGTCTTAAGCCGGCAA
 ... 3580 3590 3600

SER THR LEU ASN ASP GLY GLY LEU SER ILE...
 AAGCACCTAACAAGACGGTGGCTTGCTCTAT...
 3610 3620 3630 ...
 ... LYS ASN PRO THR GLY SER GLU GLN ILE GLN
 ...TAACAAACCCACCTGGTAGCGAACAATCCA
 ... 3640 3650 3660

FIG.21S

VAL GLY ALA ASP GLY VAL LYS PHE ALA LYS...
 AGTCGGTGCCTGATGGCGTGTAAGTTTGCCAA ...
 3670 3680 3690 ...
 ... VAL ASN ASN GLY VAL VAL GLY ALA GLY
 ...GGTTAATAATAATGGTGTTGTAGGTGCTGG
 ... 3700 3710 3720

ILE ASP GLY THR THR ARG ILE THR ARG ASP...
 CATGTGGCACACACTCGCATTACCAGAGA ...
 3730 3740 3750 ...
 ... GLU ILE GLY PHE THR GLY THR ASN GLY SER
 ...TGAATAATGGCTTTACTGGGACTAATGGCTC
 ... 3760 3770 3780

LEU ASP LYS SER LYS PRO HIS LEU SER LYS...
 ACTGTATAAAGCAAAACCCCACTAAGCAA ...
 3790 3800 3810 ...
 ... ASP GLY ILE ASN ALA GLY GLY LYS ILE
 ...AGACGGCATTAACGCAGGTGGTA AAAAGAT
 ... 3820 3830 3840

THR ASN ILE GLN SER GLY GLU ILE ALA GLN...
 TACCAACATTCAATCAGGTGAGATTGCCCA ...
 3850 3860 3870 ...

FIG.21T

... ASN SER HIS ASP ALA VAL THR GLY GLY LYS
 ...A A C A G C C A T G A T G C T G T G A C A G G C G G C A A
 ... 3880 3890 3900

ILE TYR ASP LEU LYS THR GLU LEU GLU ASN...
 G A T T A T G A T T A A A A C C G A A C T T G A A A ... 3920
 ... 3930 ...
 ... LYS ILE SER SER THR ALA LYS THR ALA GLN
 ...C A A A T C A G C A G T A C T G C C A A A A C A G C A C A
 ... 3940 3950 3960 164/183

EcoR I

ASN SER LEU HIS GLU PHE SER VAL ALA ASP...
 A A C T C A T T A C A C G A A T T C T C A G T A G C A G A ...
 3970 3980 3990 ...

... GLU GLN GLY ASN ASN PHE THR VAL SER ASN
 ...T G A C A A G G T A A T A A C T T T A C G G T T A G T A A
 ... 4000 4010 4020

PRO TYR SER SER TYR ASP THR SER LYS THR...
 C C C T T A C T C C A G T T A T G A C A C C T C A A G A C ...
 4030 4040 4050 ...

FIG.21U

```

... SER ASP VAL ILE THR PHE ALA GLY GLU ASN
...CTCTGATGTCATCATCACCCTTTGCAGGTGAAAA 4080
... 4060 4070

GLY ILE THR THR LYS VAL ASN LYS GLY VAL...
CGGCATTACCACCAAGGTAAATAAAGGTGT... 4090
... 4110 ...
... VAL ARG VAL GLY ILE ASP GLN THR LYS GLY
...GGTGCGTGTTGGGCATTGACCAACCAAGG 4140
... 4120 4130

LEU THR THR PRO LYS LEU THR VAL GLY ASN...
CTTAAACCAAGCCTAAGCTGACCGTGGGTAA... 4150
... 4160 4170 ...
... ASN ASN GLY LYS GLY ILE VAL ILE ASP SER
...TAATAATGGCAAGGCATTGTCTATTGACAG 4200
... 4180 4190

GLN ASN GLY GLN ASN THR ILE THR GLY LEU...
CCAAAATGGTCAAAATACCATCACAGGACT... 4220
... 4230 ...
... SER ASN THR LEU ALA ASN VAL THR ASN ASP
...AAGCAACACTCTAGCTAATGTTACCAATGA 4260
... 4240 4250

```

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FIG.21V

```

    LYS  GLY  SER  VAL  ARG  THR  THR  GLU  GLN  GLY...
    T A A G G T A G C G T A C G C A C C A G A A C A G G G ...
    4270                                     4280 ...
           ...  ASN  ILE  ILE  LYS  ASP  GLU  ASP  LYS  THR  ARG
           ...C A A T A T A A G A C G A G A C A A A A C C C G
           ...                                     4300
    4310                                     4320

    ALA  ALA  SER  ILE  VAL  ASP  VAL  LEU  SER  ALA...
    T G C C G C C A G C A T T G T T G A T G T G C T A G C G C ...
    4330                                     4340
           ...  GLY  PHE  ASN  LEU  GLN  GLY  ASN  GLY  GLU  ALA
           ...A G G C T T T A A C T T G C A A G G C A A T G G T G A A G C
           ...                                     4360
    4370                                     4380

    VAL  ASP  PHE  VAL  SER  THR  TYR  ASP  THR  VAL...
    G G T T G A C T T T G T C T C C A C T T A T G A C A C C G T ...
    4390                                     4400
           ...  ASN  PHE  ALA  ASP  GLY  ASN  ALA  THR  THR  ALA
           ...C A A C T T T G C C G A T G G C A A T G C C A C C A C C G C
           ...                                     4420
    4430                                     4440

    LYS  VAL  THR  TYR  ASP  THR  SER  LYS  THR...
    T A A G G T G A C C C T A T G A T G A C A C A G C A A A A C ...
    4450                                     4460
    4470 ...

```

FIG.21W

```

... SER LYS VAL VAL TYR ASP VAL ASN VAL ASP
...CAGTAAAGTGGTCTATGATGTC AATGTGGA
... 4480 4490 4500

ASP THR THR ILE GLU VAL LYS ASP LYS LYS...
TGATACAACCATTTGAAGTTAAAGATAAA ...
4510 4520 4530 ...

... LEU GLY VAL LYS THR THR THR LEU THR SER
...ACTTGGCGGTAA A A C C A C C A C A T T G A C C A G
... 4540 4550 4560 167/183

THR GLY THR GLY ALA ASN LYS PHE ALA LEU...
TAC TGG CACAGGTGCTAATAATAATTGCCCC T ...
4570 4580 4590 ...

... SER ASN GLN ALA THR GLY ASP ALA LEU VAL
...AAGCAATCAAGCTACTGGCGGATGCGCTTGT
... 4600 4610 4620

EcoR V
LYS ALA SER ASP ILE VAL ALA HIS LEU ASN...
CAGGCCAGT GATATC GTTGTCTCATCTAA A ...
4630 4640 4650 ...

```

FIG.21X

```

...   THR   LEU   SER   GLY   ASP   ILE   GLN   THR   ALA   LYS
...CACCCTTATCTGGCGACATCCAAACTGCCAA
...
4660
4670
4680

GLY   ALA   SER   GLN   ALA   ASN   SER   ALA   GLY...
AGGGGCAAGCCAAAGCGAACAACCTCAGCAGG ...
4690
4700
4710 ...
...   TYR   VAL   ASP   ALA   ASP   GLY   ASN   LYS   VAL   ILE
...CTATGTGGATGCTGATGGCAATAAGGTCA T
4720
4730
4740
4750
4760
4770 ...
4780
4790
4800

TYR   ASP   SER   THR   ASP   ASN   LYS   TYR   TYR   GLN...
CTATGACAGTACC GATAAACAAGTACTATCA ...
4750
4760
4770 ...
4780
4790
4800

LYS   GLU   VAL   ALA   LYS   ASP   LYS   LEU   VAL   ALA...
CAAGAAGTGGCCAAAGACAAACTGGTCGC ...
4810
4820
4830 ...
...   GLN   ALA   GLN   THR   PRO   ASP   GLY   THR   LEU   ALA
...CCAGCCCAAACCCAGATGGCACCATGGCC
4840
4850
4860

```

FIG.21Y

```

GLN MET ASN VAL LYS SER VAL ILE ASN LYS...
T C A A A T G A A T G T C A A A T C A G T C A T T A A C A A ...
4870                                     4880 ...
... GLU GIN VAL ASN ASP ALA ASN LYS LYS GIN
...A G A C A A G T A A A T G A T G C C C A A T A A A A A G C A
4900                                     4910 4920
...

GLY ILE ASN GLU ASP ASN ALA PHE VAL LYS...
A G G C A T C A A T G A A G A C A A C G C C T T T G T T A A ...
4930                                     4940 4950 ...
... GLY LEU GLU LYS ALA ALA SER ASP ASN LYS 169/183
...A G G A C T T G A A A A A G C C G C T T C T G A T A A C A A
4960                                     4970 4980
...

THR LYS ASN ALA ALA VAL THR VAL GLY ASP...
A A C C A A A A C G C C G C A G T A A C T G T G G T G A ...
4990                                     5000 5010 ...
... LEU ASN ALA VAL ALA GIN THR PRO LEU THR
...T T T A A A T G C C G T T G C C C A A A C A C C G C T G A C
5020                                     5030 5040
...

PHE ALA GLY ASP THR GLY THR THR ALA LYS...
C T T T G C A G G G G A T A C A G G C A C A C G C T A A ...
5050                                     5060 5070 ...

```

FIG.21Z

```

... LYS LEU GLY GLU THR LEU THR ILE LYS GLY
...A A A C T G G G C G A G A C T T T G A C C A T C A A A G G
... 5080 5090 5100

GLY GLN THR ASP THR ASN LYS LEU THR ASP...
T G G G C A A C A G A C A C C A A T A A G C T A A C C G A ...
5110 5120 5130 ...
... ASN ASN ILE GLY VAL VAL ALA GLY THR ASP
...T A A T A A C A T C G G T G T G G T A G C A G G T A C T G A
5140 5150 5160 170/183

GLY PHE THR VAL LYS LEU ALA LYS ASP LEU...
T G G C T T C A C T G T C A A A C T T G C C A A A G A C C T ...
5170 5180 5190 ...
... THR ASN LEU ASN SER VAL ASN ALA GLY GLY
...A A C C A A T C T T A A C A G C G T T A A T G C A G G T G G
5200 5210 5220

THR LYS ILE ASP ASP LYS GLY VAL SER PHE...
C A C C A A A A T T G A T G A C A A A G G C G T G T C T T T ...
5230 5240 5250 ...
... VAL ASP SER SER GLY GLN ALA LYS ALA ASN
...T G T A G A C T C A A G C G G T C A A G C C A A A G C A A A
5260 5270 5280

```

FIG.21A'

THR PRO VAL LEU SER ALA ASN GLY LEU ASP...
 C A C C C T G T G C T A A G T G C C A A T G G G C T G G A ...
 5290 5300 5310 ...
 ... LEU GLY GLY LYS VAL ILE SER ASN VAL GLY
 ... C C T G G G T G G C A A G G T C A T C A G T A A T G T G G G
 ... 5320 5330 5340

LYS GLY THR LYS ASP THR ASP ALA ALA ASN...
 C A A G G C A C A A A G A T A C C G A C G C T G C C A A ...
 5350 5360 5370 ...
 ... VAL GLN GLN LEU ASN GLU VAL ARG ASN LEU
 ... T G T A C A C A G T T A A C G A A G T A C G C A A C T T
 ... 5380 5390 5400

LEU GLY LEU GLY ASN ALA GLY ASN ASP ASN...
 G T T G G G T C T T G G T A A T G C T G G T A A T G A T A A ...
 5410 5420 5430 ...
 ... ALA ASP GLY ASN GLN VAL ASN ILE ALA ASP
 ... C G C T G A C G G C A A T C A G G T A A A C A T T G C C G A
 ... 5440 5450 5460

ILE LYS LYS ASP PRO ASN SER GLY SER SER...
 C A T C A A A A G A C C C A A A T T C A G G T T C A T C ...
 5470 5480 5490 ...

FIG.21B'

... SER ASN ARG THR VAL ILE LYS ALA GLY THR
 ...A T C T A A C C G C A C T G T C A T C A A A G C A G G C A C
 ... 5500 5510 5520

possible truncation site 2

VAL LEU GLY GLY LYS GLY ASN ASN ASP THR...
 G G T A C T T G G C G G T A A A G G T A A T A A C G A T A C ...
 5530 5540 5550 ...

... GLU LYS LEU ALA THR GLY GLY ILE GLN VAL
 ...C G A A A A C T T G C C A C T G G T G G T A T A C A A G T
 ... 5560 5570 5580

GLY VAL ASP LYS ASP GLY ASN ALA ASN GLY...
 G G G C G T G G A T A A A G A C G G C A A C G C T A A C G G ...
 5590 5600 5610 ...

... ASP LEU SER ASN VAL TRP VAL LYS THR GLN
 ...C G A T T T A A G C A A T G T T T G G G T C A A A C C C A
 ... 5620 5630 5640

LYS ASP GLY SER LYS LYS ALA LEU ALA...
 A A A G A T G G C A G C A A A A A G C C C T G C T C G C ...
 5650 5660 5670 ...

FIG.21C'

```

...   THR   TYR   ASN   ALA   ALA   GLY   GLN   THR   ASN   TYR
...C A C T T A T A C G C C G C A G G T C A G A C C A C T A
...
5680
5690
5700

LEU   THR   ASN   ASN   PRO   ALA   GLU   ALA   ILE   ASP...
T T T G A C C A A C A C C C G C A G A G C C A T T G A ...
5710
5720
5730 ...

...   ARG   ILE   ASN   GLU   GLN   GLY   ILE   ARG   PHE   PHE
...C A G A A T A A A T G A A C A A G G T A T C C G C T T C T T
5740
5750
5760
173/183

HIS   VAL   ASN   ASP   GLY   ASN   GLN   GLU   PRO   VAL...
C C A T G T C A A C G A T G G C A A T C A A G A G C C T G T ...
5770
5780
5790 ...

...   VAL   GLN   GLY   ARG   ASN   GLY   ILE   ASP   SER   SER
...G G T A C A A G G G C G T A A C G G C A T T G A C T C A A G
5800
5810
5820

Dra III

ALA   SER   GLY   LYS   HIS   SER   VAL   ALA   ILE   GLY...
T G C C T C A G G C A A G C A C T C A G T G G C C G A T A G G ...
5830
5840
5850 ...

```

FIG.21D'

```

... PHE GLN ALA LYS ALA ASP GLY GLU ALA ALA
...T T C C A G G C C A A G G C A G A T G G T G A A G C C G C
... 5860 5870 5880

VAL ALA ILE GLY ARG GLN THR GLN ALA GLY...
C G T G C C A T A G G C A G A C A A C C C A A G C A G G ...
5890 5910 ...

... ASN GLN SER ILE ALA ILE GLY ASP ASN ALA
...C A A C C A A T C C A T C G C C A T C G G T G A T A C G C
... 5920 5930 5940 174/183

GLN ALA THR GLY ASP GLN SER ILE ALA ILE...
A C A G C C A C G G G C G A T C A A T C C A T C G C C A T ...
5950 5960 5970 ...

possible truncation site 3
... GLY THR GLY ASN VAL VAL ALA GLY LYS HIS
...C G G T A C A G G C A A T G T G G T A G C A G G T A G C A
... 5980 5990 6000

SER GLY ALA ILE GLY ASP PRO SER THR VAL...
C T C T G G T G C C A T C G G C G A C C C A A G C A C T G T ...
6010 6020 6030 ...

```

FIG.21E'

```

... LYS ALA ASP ASN SER TYR SER VAL GLY ASN
...TAGGCTGATAACAGTTACAGTGTGGGTTAA
...
6040
6050
6060

ASN ASN GLN PHE THR ASP ALA THR GLN THR...
TAACACCAAGTTTACCGATGCCACTCAAC ...
6070
6080
6090 ...
... ASP VAL PHE GLY VAL GLY ASN ASN ILE THR
...CGATGTCCTTTGGTGTGGGCAATAACATCAC
...
6100
6110
6120
175/183

VAL THR GLU SER ASN SER VAL ALA LEU GLY...
CGTGACCGAAGTAAC TCGGTTGCCCTTAGG ...
6130
6140
6150 ...
... SER ASN SER ALA ILE SER ALA GLY THR HIS
...TTCAAAC TCTGCCATCAGTGCAAGGCACACA
...
6160
6170
6180

ALA GLY THR GLN ALA LYS LYS SER ASP GLY...
CGCAGGCACACAGCCAAAATACTGACGG ...
6190
6200
6210 ...
... THR ALA GLY THR THR THR THR ALA GLY ALA
...CACAGCAGGTACAAACCACCAAGCAGGTGC
...
6220
6230
6240

```

FIG.21F'

```

THR  GLY  THR  VAL  LYS  GLY  PHE  ALA  GLY  GLN...
AACCGGTACGGTTAAAGGCTTTGCTGGACA ...
6250                               6260
...   THR  ALA  VAL  GLY  ALA  VAL  SER  VAL  GLY  ALA
...AACGGCGGTTGGTGCGGTCCTCCGTGGGTGC
6280                               6290
...                               6300

SER  GLY  ALA  GLU  ARG  ARG  ILE  GLN  ASN  VAL...
CTCAGGTGCTGACGCCGTATCCAAATGT ...
6310                               6320
...   ALA  ALA  GLY  GLU  VAL  SER  ALA  THR  SER  THR
...GGCAGCAGGTGAGGTCAAGTGCCACCAAGCAC
6340                               6350
...                               6360

ASP  ALA  VAL  ASN  GLY  SER  GLN  LEU  TYR  LYS...
CGATGCGGTCAATGGTAGCCAGTTGTACA ...
6370                               6380
...   ALA  THR  GLN  SER  ILE  ALA  ASN  ALA  THR  ASN
...AGCCACCCCAAAGCATTGCCCAACCAACCA
6400                               6410
...                               6420

GLU  LEU  ASP  HIS  ARG  ILE  HIS  GLN  ASN  GLU...
TGAGCTTGACCATCGTATCCACCACCAACGA ...
6430                               6440
...                               6450

```

FIG.21G'

```

... ASN LYS ALA ASN ALA GLY ILE SER SER ALA
...A A T A A G G C C A A T G C A G G G A T T C A T C A G C
... 6460 6470 6480

MET ALA MET ALA SER MET PRO GLN ALA TYR...
G A T G G C G A T G G C G T C C A T G C C A C A A G C C T A ...
6490 6500 6510 ...
... ILE PRO GLY ARG SER MET VAL THR GLY GLY
...C A T T C C T G G C A G A T C C A T G G T T A C C G G G G
... 6520 6530 6540 177/183

ILE ALA THR HIS ASN GLY GLN GLY ALA VAL...
T A T T G C C A C C C A C A A C G G T C A A G G T G C G G T ...
6550 6560 6570 ...
... ALA VAL GLY LEU SER LYS LEU SER ASP ASN
...G G C A G T G G G A C T G T C G A A G C T G T C G G A T A A
... 6580 6590 6600

GLY GLN TRP VAL PHE LYS ILE ASN GLY SER...
T G G T C A A T G G G T A T T T A A A A T C A A T G G T T C ...
6610 6620 6630 ...
... ALA ASP THR GLN GLY HIS VAL GLY ALA ALA
...A G C C G A T A C C C A A G G C C A T G T A G G G C C G C
... 6640 6650 6660

```

FIG. 21H,

VAL GLY ALA GLY PHE HIS PHE ***

AGTTGGTGCAAGGTTTCTCACTTTTAAGCCAT ...
6670 6680 6690 ...

...AATCGCAAGATTCTTAAATCAATC
... 6700 6710 6720

TCACCATAGTTGTATAAACAGCATCAGCA ...
6730 6740 6750 ...
...TCAGTCATATTA CTGATGCTGATGTTT
... 6760 6770 6780 6783

ATCACTTAACCATTTACCGCTCAAGTGA ...
6790 6800 6810 ...
...TTCCTCTTCACCATGACCAAAATCGCCATTG
... 6820 6830 6840

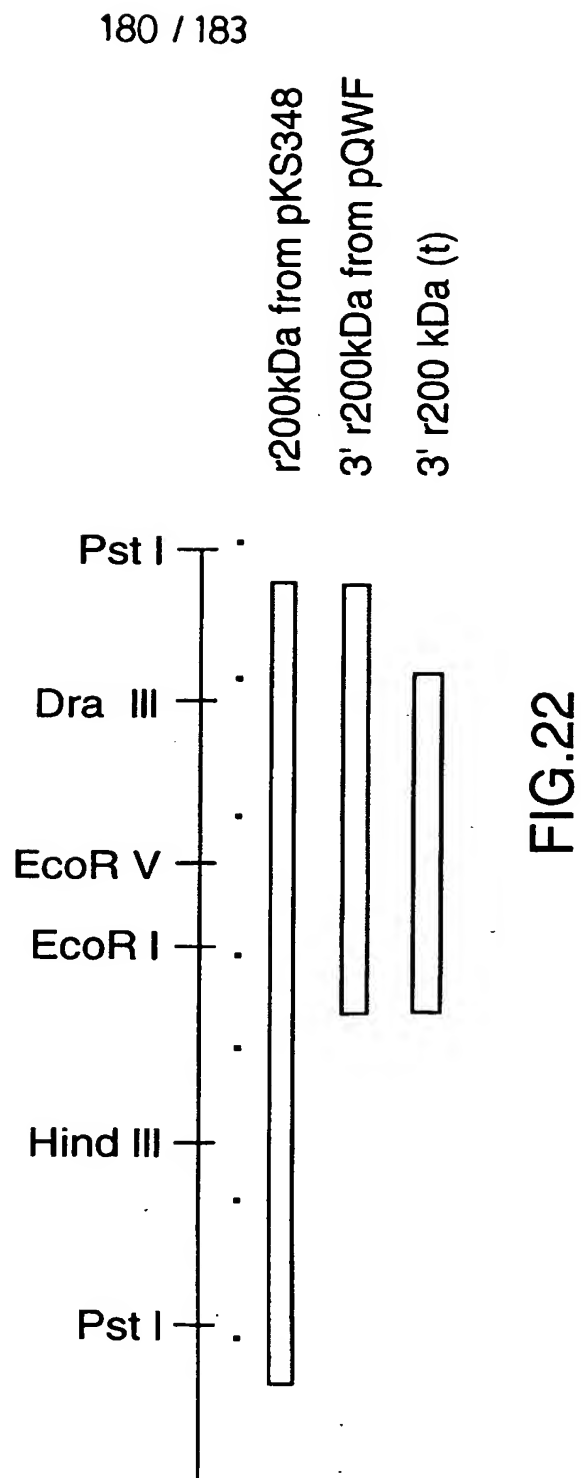
ATCATAGGTAACCTTATTGAGTAAATTTA ...
 6850 6860 6870 ...
 ...TCAATGTTAGTTAGTATGGTTAAATT
 ... 6880 6890 6900

FIG.21'

GTGCCATTGACCAAAATGACCGATTAT ...
6910 6920 6930 ...
...CCCGAAATTTCTGATTATGATCCGTTGAC
6940 6950 6960

Pst I
CTGCAGGTCGAC
6970

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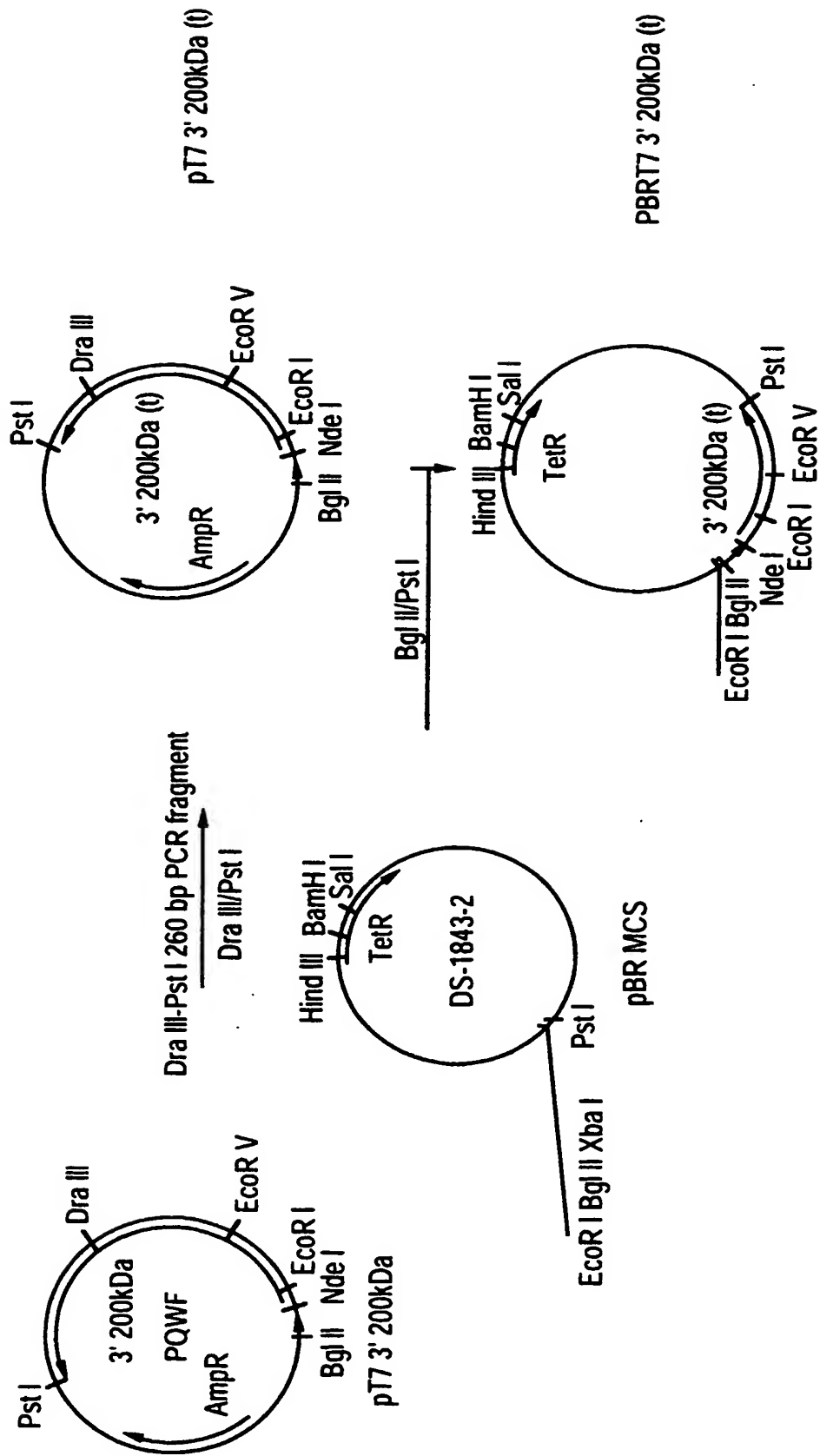


FIG.23A

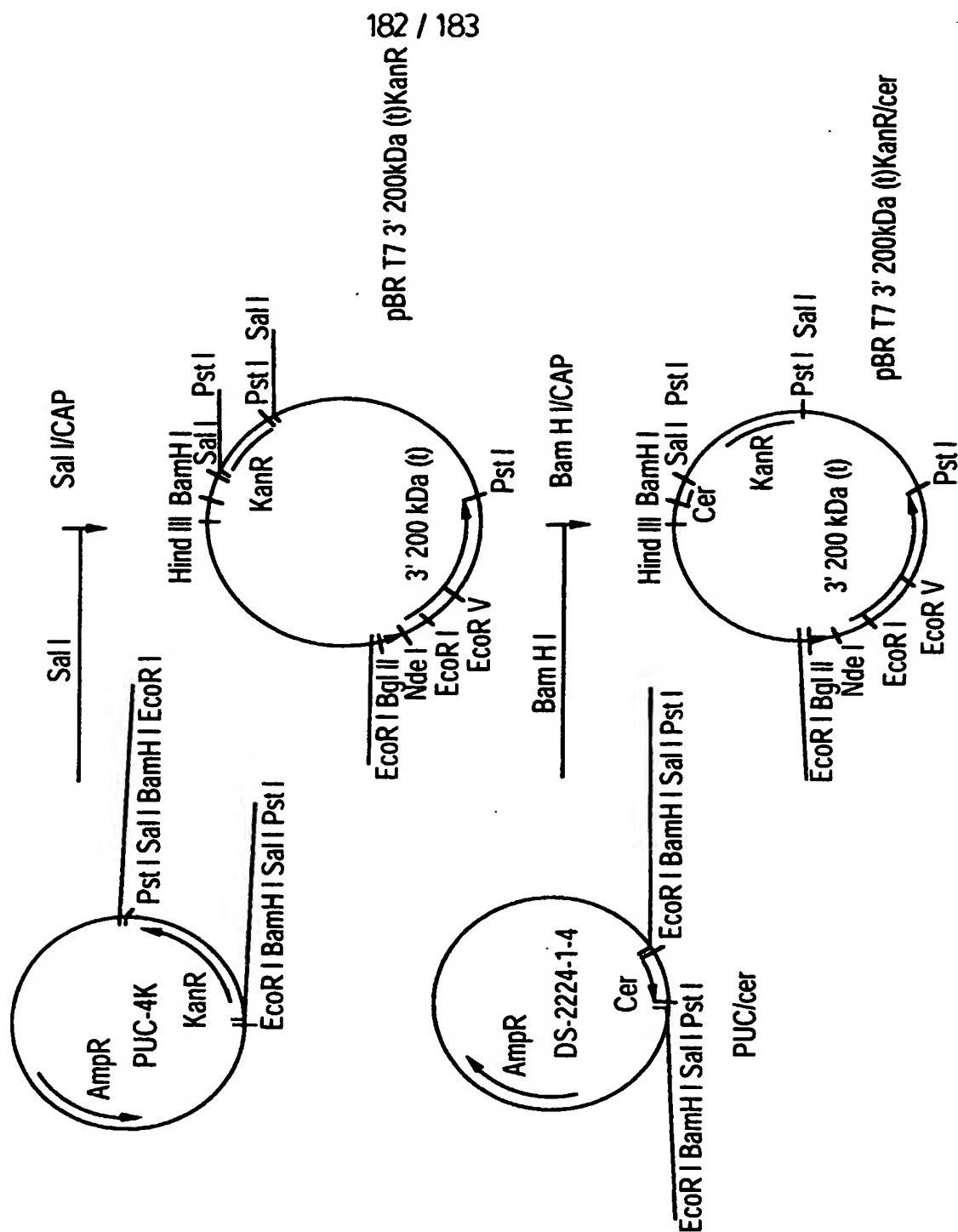
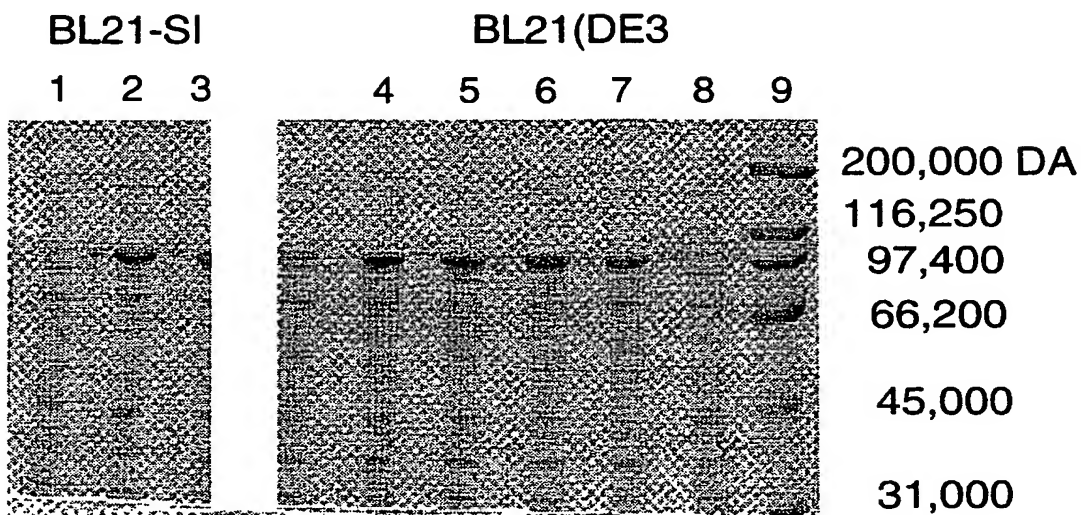


FIG.23B

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Expression of 3' r200 kDa (t) from E. coli



LANE 1 OA54-2-7-1 t0

LANE 2 OA54-1-6-1 t4

LANE 3 OA54-2-7-1 t4

LANE 4 OA54-2-7-2 t4

LANE 5 OA54-2-7-1 t4

LANE 6 OA54-1-6-2 t4

LANE 7 OA54-1-6-1 t4

LANE 8 OA54-1-6-2 t0

LANE9 molecular weight markers

FIG.24

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